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Rhomboidia wuliangshanensis gen. & sp. nov.
(Xu & al.— FIG. 2, p. 657)

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LORELEI L. NORVELL

editor@mycotaxon.com

Pacific Northwest Mycology Service
6720 NW Skyline Boulevard
Portland, Oregon 97229-1309 USA

NOMENCLATURE EDITOR

SHAUN R. PENNYCOOK

PennycookS@LandcareResearch.co.nz

Manaaki Whenua Landcare Research
Auckland, New Zealand

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MYCOTAXON

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The Editors express their appreciation to the following individuals who have, prior to acceptance for publication, reviewed one or more of the papers prepared for this issue.

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p.174, Acknowledgments

for: The author would like to thank Prof. Dr. Ertuğrul Sesli, Prof. Dr. İbrahim Türkekul, and Dr. Shaun Pennycook for their helpful comments and careful review.

read: The author would like to thank **Yüzüncü Yıl Üniversity, Coordination of Scientific Research Projects for financial support (2010-FED-B031 and FYL-2016-5213) and** Prof. Dr. Ertuğrul Sesli, Prof. Dr. İbrahim Türkekul, and Dr. Shaun Pennycook for their helpful comments and careful review.

Mycotaxon 134-3

p. vii, line 21 for: *Marthamyces culmigenus* (Ellis & Everh.) P.R. Johnst.
read: *Marthamyces culmigenus* (Ellis & **Langl.**) P.R. Johnst.

p.496, lines 3–5

for: *Marthamyces culmigenus* (Ellis & Everh.) P.R. Johnst., comb. nov.
IF 556322
≡ *Naemacyclus culmigenus* Ellis & Everh.,
Proc. Acad. Nat. Sci. Philadelphia 45: 151, 1893.

read: *Marthamyces culmigenus* (Ellis & **Langl.**) P.R. Johnst., comb. nov.
IF 556322
≡ *Naemacyclus culmigenus* Ellis & **Langl., in Ellis & Everhart,**
Proc. Acad. Nat. Sci. Philadelphia 45: 151, 1893.

[**Semi-bold** fonts used above to flag corrected terms.]

Corrigenda in current issue (134–4)

Cited below are mistakes or oversights present in approved input files not detected by authors until after PDF conversion.

p. 613: Pu Liu and fellow coauthors wish to acknowledge the contributions made to "Dictyostelids from Jilin Province, China 3: new *Cavenderia* and *Dictyostelium* records" (Mycotaxon 134: 613–618) by Prof. Zhuang Li (Shandong Provincial Key Laboratory for Biology of Vegetable Diseases and Insect Pests, College of Plant Protection, Shandong Agricultural University, Tai'an 271018, China). The author sequence originally intended should read "Pu Liu, Shunhang Zhang, Zhuang Li, Yue Zou, Xueping Kang, Yu Li."

p.669, line 26 for: MK43983
read: MK439830

From the Editor-in-Chief

Deadlines, Mycotaxon & Nomenclature—The most onerous task your esteemed *Editor-in-Chief* faces is bringing the year-end issue in 'on time.' A glance at our publication history suggests that during her tenure, she has failed miserably. Since 2004, she has met only three of her sixteen December deadlines: New Year's Eve 2004, Boxing Day 2007, 30 December 2009. Given this deplorable 37% success rate, it is no surprise that, once again, an October-December Mycotaxon will appear in January. (It could be worse: after adopting electronic submission and new software, we released the last 2005 volume on 11 May 2006!)

Reasons/excuses for delays are myriad: time-consuming nomenclatural revision and editorial repair of sloppily prepared submissions (on the misplaced notion that it is quicker for us to do authors' work for them), outside research commitments, severe health problems, uncontrollable press delays. Nonetheless, this year we were convinced that Mycotaxon 134(4) would be ready for delivery well before 2020.

What we did not anticipate was the small number of research papers submitted. With several authors not sending us their final papers after their 2019 nomenclatural review, we waited until December 27 before deciding to release the issue with only 140 pages (the smallest issue EVER since 1974) rather than waiting for final submissions that have yet to appear. Frustrating, because removal of required page charges produced a flood of 138 accessions during 2019.

What makes the year-end release date so important to Mycotaxon? With nomenclatural priority date-based, the date of publication is dictated by the actual release date and not what is displayed on the cover. That means that taxonomic names published in periodicals must cite both the actual date of publication and the 'nominal' date printed in the issue, e.g., following the order, *Haematomma pluriseptatum* R. Tang, Mycotaxon 134: 638 (2020) but indexed as "Miao, C, Tang R, Dong L, Ren Z, Zhao Z. 2020 ('2019'). *Haematomma pluriseptatum* sp. nov. from China. Mycotaxon 134: 637–641. https://doi.org/10.5248/134.637 " Much less confusing and infinitely more restful to have only ONE date to cite!

Mycotaxon 134(4) presents 15 papers by 81 authors (representing 15 countries) as revised by 34 expert reviewers and the editors.

The 2019 October–December Mycotaxon proposes one new genus (*Rhomboidia* from China) and eight new species representing *Bactrodesmium* from Ecuador; *Dendrographium, Filsoniana*, *Haematomma,* and *Rhomboidia* from China; *Exserticlava* from Brazil; *Leucoagaricus* from Pakistan; and *Urocystis* from the U.S.A. We also offer a new combination in *Puccinia* and epitypification for *Puccinia caulophylli.*

New species range extensions are reported for [ascomycetes] *Aureobasidium, Sarcophoma, Stigmina* in Turkey and new records and hosts of fern-associated ascos in eastern Mexico and [myxomycetes] *Cavenderia, Dictyostelium,* and *Didymium* in China.

Two papers on *Sarcopodium* [1] explain why *S. flocculentum* is the correct name for *S. macalpinei* and [2] discuss the first sexual morph recorded for *S. vanillae* in Thailand. Another paper treats the full life cycle for the rust *Puccinia* (≡ *Aecidium*) *caulophylli.*

Our small year-end issue closes with the announcements of two mycobiota [recently posted on www.mycotaxon.com] covering [1] new records of ascomycetes on *Syagrus coronata* in Brazil's Caatinga biome and [2] dark- and pink-spored agarics in Bolivia.

Wishing us all health, happiness, illumination, and peace in 2020,

Lorelei L. Norvell (*Editor-in-Chief*)
8 January 2020

publication date for volume one hundred thirty-four (3)

Mycotaxon for July–September 2019 (i–xiv + 423–590)
was issued on October 2, 2019

2020 Mycotaxon submission procedure

Prospective Mycotaxon authors should download the Mycotaxon 2020 guide, review & submission forms, and Mycotaxon sample manuscript by clicking the 'file download page' link on our Instructions to Authors page before preparing their manuscript. This page briefly summarizes our '4-step' submission process.

1—Peer review: Authors first contact peer reviewers (two for journal papers; three for mycobiota/fungae) before sending them formatted text & illustration files and the appropriate 2020 Mycotaxon journal or mycota reviewer comment form. Experts return revisions & comments to both the *Editor-in-Chief* <editor@mycotaxon.com> and authors. All co-authors must correct and *proof-read* their files before submitting them to the *Nomenclature Editor*.

2—Nomenclatural review: Authors email all **error-free** text & illustration files to the *Nomenclature Editor* <PennycookS@LandcareResearch.co.nz>. Place **first author surname** + **genus** + 'Mycotaxon' on the subject line, and (required) attach a completed submission form. The Nomenclature Editor will (i) immediately assign the accession number and (ii) after a few weeks return his notes and suggested revisions to the author(s) and *Editor-in-Chief*.

3—Final submission: All coauthors thoroughly revise and proof-read files to prepare error-free text and images ready for immediate publication. Poorly formatted copy will be rejected or returned for revision. E-mail the final manuscript to the *Editor-in-Chief* <editor@mycotaxon.com>, adding the **accession number** to the message and **all** files, which include a **(i)** revised 2020 submission form, all **(ii)** text files and **(iii)** jpg images, and **(iv)** FN, IF, or MB identifier verifications for each new name or typification. The *Editor-in-Chief* acknowledges submissions within two weeks of final submission but requests authors to wait at least 14 days before sending a follow-up query (without attachments).

4—Final editorial review & publication: The *Editor-in-Chief* conducts a final grammatical and scientific review and returns her editorial revisions to all expert reviewers and coauthors for final author approval. Author-approved files are placed in the publication queue.

The PDF proof and bibliographic & nomenclatural index entries are sent to all coauthors for final inspection. After PDF processing, the *Editor-in-Chief* corrects only PDF editorial/conversion and index entry errors; corrections of all other errors are listed in the Errata of a subsequent issue for no charge. Authors will pay fees for mycobiota uploads, optional open access, and correction of major author errors to the *Business Manager* <subscriptions@mycotaxon.com> at this time.

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Urocystis cumminsii sp. nov., a smut fungus on *Themidaceae* from Arizona

Kyryll G. Savchenko[1]*, Sylena R. Harper[2],
Lori M. Carris[2], Lisa A. Castlebury[3]

[1] *Department of Biological Sciences, Butler University, Indianapolis, IN 46208*

[2] *Department of Plant Pathology, Washington State University, Pullman, WA 99164, USA*

[3] *USDA-ARS, Mycology and Nematology Genetic Diversity and Biology Laboratory, 10300 Baltimore Ave, Beltsville, MD 20705, USA*

* Correspondence to: *ksavchen@butler.edu*

Abstract—The morphology and phylogenetic relationships of a species of *Urocystis* on *Dichelostemma capitatum* (*Themidaceae*, *Asparagales*) collected in the Tucson Mountains in Arizona, United States, were studied using microscopy and ITS rDNA sequence analyses. This is a first record for smut fungi on hosts from *Themidaceae.* Molecular phylogenetic analyses based on ITS sequence data revealed its basal position in relation to species on *Poaceae.* As a result, the smut in leaves of *Dichelostemma capitatum* is described and illustrated here as a new species, *Urocystis cumminsii.*

Key words—plant pathogens, taxonomy *Urocystidales*

Introduction

Urocystis Rabenh. ex Fuckel contains more than 170 species of plant pathogenic smut fungi, found all over the world but more common in temperate areas of both hemispheres (Vánky 2011b). More than 60% of *Urocystis* species are found on monocotyledons, with *Poaceae* serving as a major monocotyledonous host family, followed by *Juncaceae*, *Hypoxidaceae*, *Convallariaceae*, *Amaryllidaceae*, and *Hyacinthaceae* (Vánky 2011b). The intra-level phylogenetic relationships of *Urocystis* species have never been analysed and thus far only the graminicolous species from triticoid hosts

have been included in comprehensive phylogenetic analyses (Savchenko & al. 2017). Most of the *Urocystis* species described recently—e.g., *U. achnatheri* L. Guo, *U. anemones-narcissiflorae* Vánky, *U. arxanensis* L. Guo, *U. beckwithiae* Vánky, *U. circaeasteri* Vánky, *U. dunhuangensis* S.H. He & L. Guo, *U. glabella* Vánky & R. G. Shivas, *U. helanensis* L. Guo, *U. koeleriae* L. Guo, *U. phalaridis* Vánky, *U. puccinelliae* L. Guo & H.C. Zhang, *U. rostrariae* Piątek, *U. sinensis* L. Guo, *U. skirgielloae* Piątek, *U. wangii* L. Guo, and *U. xilinhotensis* L. Guo & H.C. Zhang—were supported only by morphological and host-specialization data (Guo 2002, 2005, 2006; Guo & Zhang 2004, 2005; He & Guo 2007; Piątek 2006a, 2006b; Vánky 2004, 2005, 2011a; Vánky & Abbasi 2011). The integration of molecular phylogenetic analyses, host plant taxonomy, and morphology provides a natural classification for various smut genera (Bauer & al. 2008; Castlebury & al. 2005; Kruse & al. 2018; Lutz & al. 2008; McTaggart & al. 2012; Savchenko & al. 2013, 2015; Vánky & Lutz 2007), justifying the need of a phylogenetic study of the genus.

During a survey of *Urocystis* species diversity in the United States, we examined a specimen identified as *Urocystis* sp. on *Dichelostemma capitatum* (Benth.) Alph. Wood (*Themidaceae*) from Arizona in the WSP herbarium. Previously, no *Urocystis* species had been recorded on hosts from this family. The present study aimed to resolve the specific status of the smut on *D. capitatum* through morphological analysis and determine its phylogenetic affinities within *Urocystis*.

Table 1. GenBank sequences used in this study.

Species	GenBank no.	Reference
Antherospora scillae	EF653983	Bauer & al. 2008
A. vaillantii	EF653988	Bauer & al. 2008
Urocystis bolivarii	KX057771	Savchenko & al. 2017
U. colchici	DQ839596	Matheny & al. 2006
U. cumminsii	MK575496	This study
U. eranthidis	JN367299	Kellner & al. 2011
U. fischeri	KF668284	Smith & Lutz 2013
U. occulta	KX057774,	Savchenko & al. 2017
U. trillii	HQ239361	Henricot 2010
U. tritici	KX057782	Savchenko & al. 2017
Ustilago hordei	AY345003	Stoll & al. 2003
Vankya heufleri	EF667965	Bauer & al. 2008
V. ornithogali	EF635910	Bauer & al. 2008

Materials & methods

The herbarium specimen is deposited in Washington State University Mycological Herbarium, Pullman, WA, United States (WSP).

Sorus and spore characteristics were studied using dried herbarium material. Specimens were examined by light microscopy (LM). Pictures of sori were taken with a Canon Power Shot G10 camera. For LM, spores were mounted in 90% lactic acid on a microscope slide, gently heated to boiling point to eliminate air bubbles, and then examined under a Carl Zeiss Axiostar™ light microscope at 1000× magnification and photographed with a Canon Power Shot G10 camera. At least 50 spore balls were measured, and the variation is presented as a range with extreme values given in parentheses. Means and standard deviations (SD) are provided after the spore size ranges.

For SEM studies, spore balls were attached to metal stubs by double-sided adhesive tape and coated with gold. Spore surface ornamentation was observed at 15 kV and photographed with a JEOL JSM-6700F scanning electron microscope with a working distance of c. 12–13 mm.

Sequences from other species of *Urocystis* and related genera were obtained from GenBank (Table 1). Genomic DNA was isolated from spore balls removed from the herbarium specimen that had been lysed in 1.5 mL tubes for 1 min using FastPrep®24. Tubes were incubated in a water bath for 5 hours at 55 °C, and DNA extracted using DNeasy Plant Mini Kit (QIAGEN) following the manufacturer's instructions.

DNA was amplified in 20 µl aliquots on an Applied Biosystems® GeneAmp 9700 thermal cycler using ITS1 as the forward primer and ITS4 as the reverse primer (White & al. 1990).

Standard cycling parameters with an annealing temperature of 57 °C were used for amplification. PCR products were purified with USB ExoSAP-IT according to the manufacturer's instructions, amplified with the forward and reverse PCR primers with the BigDye® Terminator v3.1 Cycle Sequencing Kit, and sequenced on an ABI PRISM® 3100 Genetic Analyzer.

Consensus sequences were assembled, aligned, and edited with Geneious 7.1.8 for MacOS and with MAFFT 6.853 (Katoh & al. 2002, Katoh & Toh 2008) using the L-INS-i option. Maximum Likelihood (ML) was implemented as a search criterion in RAxML (Stamatakis 2014). GTR+I+G was specified as the evolution model in MrModeltest (Nylander & al. 2004). The RAxML analyses were run with a rapid Bootstrap analysis (command –f a) using a random starting tree and 1000 maximum likelihood bootstrap replicates. A Markov Chain Monte Carlo (MCMC) search in a Bayesian analysis (BA) was conducted with MrBayes (Ronquist & Huelsenbeck 2003). Four runs were implemented for 5 million generations. The cold chain was heated to a temperature of 0.25°C. Substitution model parameters were sampled every 500 generations and trees were saved every 1000 generations. Convergence of the Bayesian analysis was confirmed using AWTY (Nylander & al. 2008) and a

burn-in of 18,000 generations was calculated. The ML and Bayesian analyses were run three times to test accuracy. The tree was rooted using *Ustilago hordei* (Pers.) Lagerh.

Results

The ITS alignment of 13 sequences (including the outgroup *Ustilago hordei*) comprised 643 characters including gaps. The different BA and ML analytical runs yielded consistent topologies in respect to well-supported branches (a posteriori probability >90% in most cases). The consensus tree of one run of Bayesian phylogenetic analyses is presented in Fig. 1. The *Urocystis* sequences fell into two major clades. The first clade comprised species from *Poaceae* and *Themidaceae*, and the second clade included species from *Cyperaceae*, *Liliaceae* s.l., and *Ranunculaceae*. The two species from the genus *Vankya* Ershad clustered together with the second *Urocystis* clade.

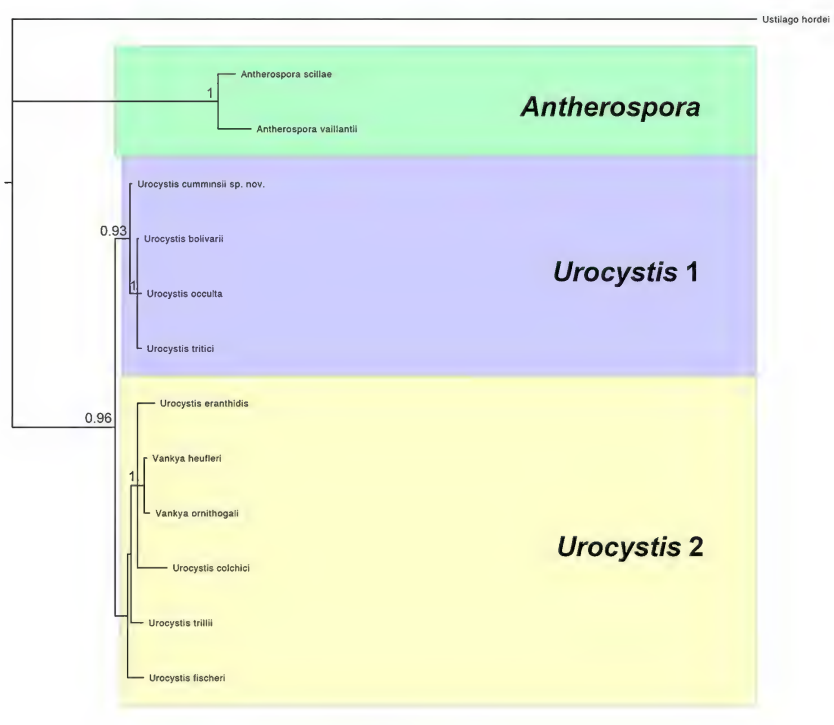

Fig. 1. Bayesian inference of phylogenetic relationships resulting from the analysis of ITS nucleotide sequence data. Numbers on branches are estimates for PPs from Bayesian inference (only probabilities >0.8 are shown).

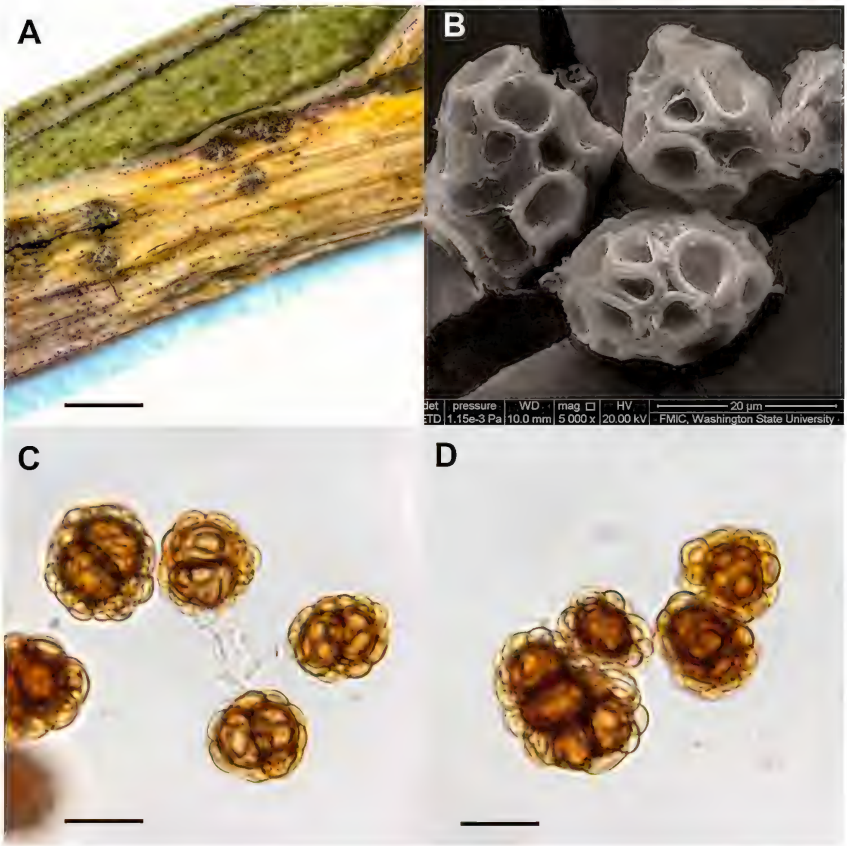

FIG. 2. *Urocystis cumminsii* (WSP 68198). A. sori in leaves of *Dichelostemma capitatum*; B. spore balls seen by SEM; C, D. spore balls seen by LM. Scale bars: A = 2 mm, B = 5 µm, C, D = 20 µm.

Taxonomy

Urocystis cumminsii K.G. Savchenko, Carris & Castl., **sp. nov.** FIG. 2

MB 830145

Differs from *Urocystis camassiae* by its lighter colored yellowish-brown spores with thicker walls and its smaller thinner walled sterile cells, and by its host specialization on *Themidaceae.*

TYPE: USA. Arizona, King's Canyon, 16 km west of Tucson, on *Dichelostemma capitatum* (as *D. pulchellum*), 30.03.1981, leg. G.B. Cummins (**Holotype,** WSP 68198; GenBank MK575496).

ETYMOLOGY: Named after George B. Cummins (1904–2007), an eminent American mycologist, who collected the holotype specimen.

Sori in leaves as slightly elevated, pustular, elongate areas of various size and shape, sometimes confluent, visible on both sides of the leaf, initially lead-colored and covered by the epidermis which ruptures exposing the powdery, black mass of spore balls. Spore balls globose, subglobose, ovoid to irregular, 20–45 µm diam., composed of 1–6 (mostly 3) spores and more or less complete investing layer of sterile cells. Spores subglobose, ovoid, irregularly oblong to elongated, 11–15 × 12–18 µm diam. [mean ± SD, 13.3 ± 2.6 × 15 ± 2.9 µm], medium yellowish brown, wall 1–1.5 µm thick, smooth. Sterile cells subglobose, elongated, ovoid, 5–7 × 5–11(–13) µm, pale yellow, to almost hyaline, with smooth, 1 µm thick wall.

Discussion

Dichelostemma Kunth is a North American genus of wild hyacinths, closely related to *Brodiaea* Sm., from the family *Themidaceae*. Plants from this family are native to Central America and western North America, from British Columbia to Guatemala (Pires & Sytsma 2002, Stevens 2018). No members of *Themidaceae* were previously known to be parasitized by smut fungi (Vánky 2011b). Our molecular phylogenetic analyses and morphological data have helped resolve the systematic position of *Urocystis* on *D. capitatum*.

The only possible close relative to *U. cumminsii* might be another native North American species, *U. camassiae* Vánky, found on *Camassia* Lindl. (*Agavaceae*; Fay & Chase 1996, Pires & Sytsma 2002). However, *U. camassiae* is distinguished by its darker colored reddish-brown spores with thinner spore walls (0.5–1 µm) and its larger (5–17 µm) sterile cells with thicker walls (1–2 (–3) µm; Vánky 1994).

ITS phylogenetic analysis infers that *U. cumminsii* is sister to the clade of *Urocystis* species on grasses and separate from species found on hosts from families more closely related to *Themidaceae*, such as *U. colchici* (Schltdl.) Rabenh. ex A.A. Fisch. Waldh. and *U. trillii* H.S. Jacks., indicating multiple inter-family host jumps during the evolution of *Urocystis* species, similar to those in the closely related genus *Thecaphora* Fingerh. (Vasighzadeh & al. 2014). Interestingly, *Vankya heufleri* (Fuckel) Ershad and *V. ornithogali* (J.C. Schmidt & Kunze) Ershad also clustered within the *Urocystis* lineage (Fig. 1).

Most sequences of *Urocystis* in GenBank are derived from the LSU region. Unfortunately, our preliminary analysis showed that LSU is not informative for *Urocystis* phylogenetics. Hence, we based our current phylogeny on ITS data, utilizing the limited number of *Urocystis* ITS sequences available in GenBank. Additional sequencing is needed to resolve the taxonomy and evolutionary

relationships within *Urocystis,* as well as the phylogenetic affiliation of closely related genera, such as *Vankya.*

Urocystis cumminsii expands the occurrence of *Urocystis* species to the host family *Themidaceae.* Future combined molecular phylogenetic and morphological analyses may reveal higher diversity among *Urocystis* species in North America.

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Leucoagaricus brunneus sp. nov. from Khyber Pakhtunkhwa, Pakistan

Zia Ullah[1&2], Sana Jabeen[2&3], Muhammad Faisal[1], Habib Ahmad[4], Abdul Nasir Khalid[2]

[1] *Department of Microbiology and Molecular Genetics &* [2]*Department of Botany: University of the Punjab, Quaid-e-Azam Campus-54590, Lahore, Punjab, Pakistan*

[3]*Department of Botany, Division of Science & Technology, University of Education, Township, Lahore, Pakistan*

[4]*Islamia College, University Peshawar, Peshawar, Pakistan*

* Correspondence to: *ziaullah.phd.mmg@pu.edu.pk*

Abstract—A field survey of macrofungi from the Hindu Kush range of District Swat revealed a fungus morphologically similar to *Leucoagaricus* but representing a new species, here named *L. brunneus*. A detailed description and comparison with closely allied taxa are provided. Maximum likelihood analysis based on the internal transcribed spacer rDNA region (ITS) confirm its placement in *Leucoagaricus* sect. *Rubrotincti*.

Key words—*Agaricaceae*, *Agaricales*, *Agaricomycetes*, phylogeny, polyphyletic

Introduction

Leucoagaricus Locq. ex Singer, assigned to the family *Agaricaceae* (Singer 1986, Vellinga 2004), is represented by over 100 species in the northern and southern hemispheres (Kumar & Manimohan 2009; Ge 2010; Liang & al. 2010; Vellinga 2010; Vellinga & Balsley 2010; Vellinga & al. 2010; Muñoz & al. 2012, 2014; Kumari & Atri 2013; Malysheva & al. 2013; Ye & al. 2014; Ge & al. 2015; Qasim & al. 2015; Dovana & al. 2017; Hussain & al. 2018; Usman & Khalid 2018). From Pakistan only ten *Leucoagaricus* species have been reported previously: *L. asiaticus* Qasim & al., *L. badius* S. Hussain & al., *L. lahorensiformis* S. Hussain

& al., *L. lahorensis* Qasim & al., *L. leucothites* (Vittad.) Wasser, *L. pabbiensis* Usman & Khalid, *L. pakistaniensis* Jabeen & Khalid, *L. serenus* (Fr.) Bon & Boiffard. *L. sultanii* S. Hussain & al., and *L. umbonatus* S. Hussain & al. (Ahmad & al. 1997, Ge & al. 2015, Qasim & al. 2015, Hussain & al. 2018, Usman & Khalid 2018). The genus is characterized morphologically by small- to medium-sized basidiomata with entire pileus margins, free lamellae, a central, equal to bulbous stipe, a membranous, persistent annulus, a white, cream, or pink spore print white, usually dextrinoid basidiospores, the presence of cheilocystidia, rare occurrence of pleurocystidia, and absence of clamp connections (Singer 1986).

Several molecular phylogenies indicate that *Leucoagaricus* is polyphyletic (Johnson & Vilgalys 1998, Johnson 1999, Vellinga 2004). Vellinga (2003, 2004) showed that *Leucoagaricus* and *Leucocoprinus* species cluster together phylogenetically but intermix within a single clade. Because of the large number of species in the clade and relatively limited molecular data, the taxonomic and phylogenetic relationships among many *Leucoagaricus* and *Leucocoprinus* species have not yet been resolved.

During the present investigation, one *Leucoagaricus* specimen collected from the Shawar Valley (district Swat, Khyber Pakhtunkhwa, Pakistan) is proposed here as a new species, *L. brunneus*, supported by our morphological and phylogenetic analyses.

Material & methods

The mushroom was collected during a forest foray in Shawar valley, Khyber Pakhtunkhwa, Pakistan, during the 2017 monsoon season and photographed at the sampling site. Macrocharacters were recorded from the fresh basidioma, with colors coded according to Munsell's Soil Color Charts (1975). The specimen was air dried for further analyses and deposited in the Herbarium of University of the Punjab, Quaid-e-Azam Campus, Lahore, Pakistan (LAH).

For microscopic studies, fruiting body tissues were mounted in 2% KOH and Congo red (to increase contrast). Basidia, basidiospores, cheilocystidia, and pellicular elements were measured using ScopeImage 9.0. DNA extraction followed Bruns (1995). The internal transcribed spacer region (ITS1–5.8S–ITS2 = ITS) was amplified with the ITS1F/ITS4 primer combination (White & al. 1990, Gardes & Bruns 1993). PCR products were purified and both strands were sequenced by Beijing Genomic Institute (BGI).

For phylogenetic analysis, an ITS consensus sequence was generated in BioEdit (Hall 1999) and BLAST searched at NCBI (https://www.ncbi.nlm.nih.gov/); closely related sequences in *L.* sect. *Rubrotincti* were retrieved from both database and literature (Hussain & al. 2018). *Lepiota subgracilis* Kühner was chosen as outgroup (Liang & al. 2010). All sequences were aligned online using PRANK tool

(https://www.ebi.ac.uk/goldman-srv/webprank/). Gaps were treated as missing data. The final aligned ITS dataset was phylogenetically analyzed through MEGA 6.0 software. Maximum Likelihood (ML) analysis was performed by selecting Kimura 2-parameter with Gamma Distributed model using Best-Fit Substitution Model approach in MEGA 6.0 (Tamura & al. 2013).

Taxonomy

Leucoagaricus brunneus Z. Ullah, Jabeen & Khalid, **sp. nov.** FIGS 1, 2

MB 827985

Differs from *Leucoagaricus truncatus* by its smaller size, smooth shiny non-squamulose pileus with brown striations, and its longer and narrower elongate to cylindrical basidiospores.

TYPE: Pakistan. Khyber Pakhtunkhwa Province, Swat district, Lower Shawar, under *Quercus oblongata* D. Don (*Fagaceae*), 8 July 2017, Zia Ullah LS4 (**Holotype**, LAH35862; GenBank MH990662).

ETYMOLOGY: *brunneus* (Latin) refers to the brown coloration of the pileus fibrils.

FIGURE. 1. *Leucoagaricus brunneus* (holotype, LAH35862). Basidioma. Scale bars = 0.5 cm.

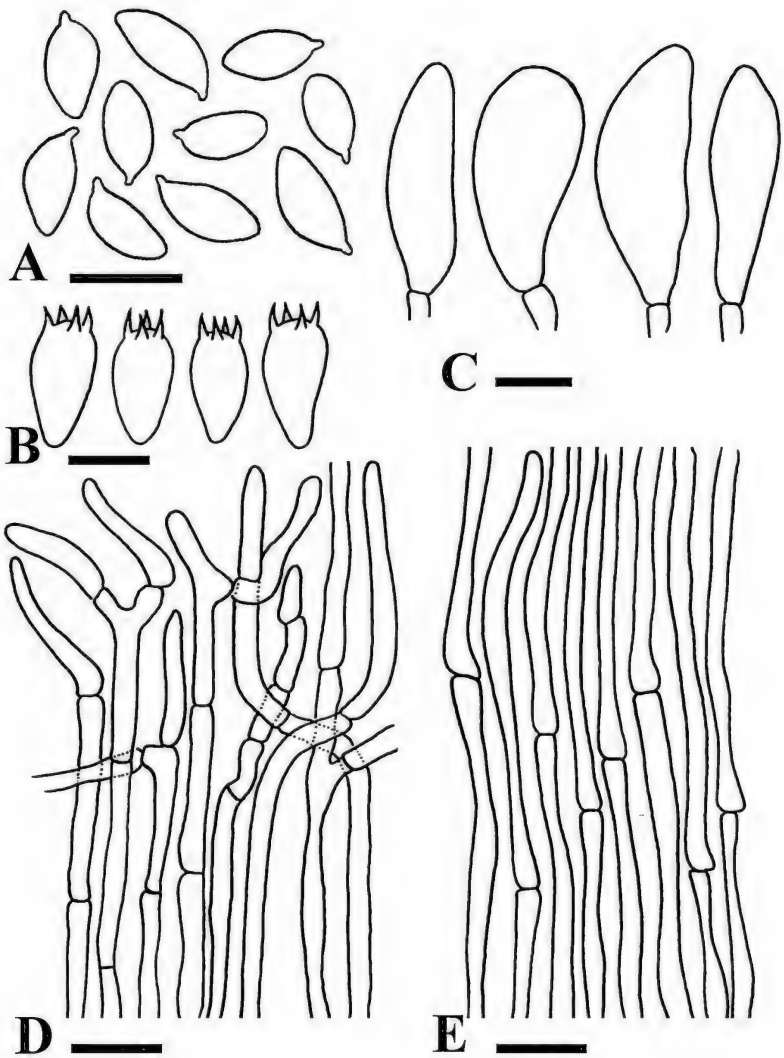

FIGURE. 2. *Leucoagaricus brunneus* (holotype, LAH35862). A. Basidiospores; B. Basidia; C. Cheilocystidia; D. Pileipellis; E. Stipitipellis. Scale bars = 10 µm. (Drawing by Sana Jabeen.)

PILEUS 35 mm diam, plane with incurved margins and umbonate center, surface smooth and shiny, dark brown (10YR1/2) from center to lighter brown (10YR2/4) towards margin in the form of radial striations, context cream.

Lamellae free, close to crowded, margins entire, cream. Lamellulae absent. Stipe central, 9 × 4–8 mm, narrower towards the apex and wider (≤8 mm) towards the base, then again narrowing (≤6 mm) at the base, cream with grayish brown (10YR4/4) patches over the central part; annulus superior (at the center of the upper half), white.

Basidiospores [30/1/1] (8.0–)8.2–10.5(–10.6) × (4–)4.1–4.9(–5.1) µm, Q = (1.8–)1.9–2.1(–2.2), avQ = 2, elongate to cylindrical in face view, amygdaliform in side view, smooth, germ pore lacking, dextrinoid in Melzer's reagent, hyaline in KOH. Basidia 17.3–19 × 7.4–8.1 µm, clavate, smooth, hyaline, 4-spored. Cheilocystidia 29.7–32.8 × 8.5–12.7 µm, clavate to subclavate, hyaline, without crystals. Pleurocystidia absent. Pileipellis a cutis with slightly clavate to cylindrical elements, 4.1–6.7 µm diam, hyaline in KOH. Stipitipellis cylindric hyphae, 3.0–5.2 µm diam, hyaline in KOH. Clamp connections absent in all tissues.

Ecology & distribution—Saprobic and solitary on humus-rich soil under *Quercus oblongata* [= *Q. incana* Roxb., nom. illeg.], at 1200 m elevation, in moist temperate *Quercus* vegetation.

Phylogenetic analysis

The 72 ITS sequence dataset (Table 1, Fig. 3) comprises 757 positions. Maximum likelihood analysis clusters the local collection in a sister clade with *L. truncatus* Z.W. Ge & Zhu L. Yang and *L. purpureolilacinus* Huijsman with a bootstrap support of 72% (Fig. 3).

Discussion

Leucoagaricus brunneus can be distinguished from *L. truncatus* based on basidioma size. *Leucoagaricus truncatus* produces medium to large (40–80 mm) basidiomata (Ge & al. 2015) and is further separated by the orange-white to gray-orange furfuraceous squamules (Ge & al. 2015) on its pileus surface in contrast to the smooth shiny pileus with brown striations that distinguish *L. brunneus*. *Leucoagaricus truncatus* is further separated microscopically by its more broadly ovoid and broadly amygdaliform basidiospores (Ge & al. 2015). The ITS sequence analysis also provides strong bootstrap support for *L. brunneus* as an independent taxon.

Leucoagaricus brunneus differs from *L. purpureolilacinus,* which is characterized by a pinkish brown pileus and presence of crystalliferous cheilocystidia (Vellinga 2001).

Pileus morphology also separates *Leucoagaricus brunneus* with its dark brown umbo and brownish striations running towards the margin from

the center from *L. serenus* and *L. crystallifer* Vellinga, both characterized by whitish basidiomata and pilei with white-to cream obtuse umbos with obvious striations near the margins. *Leucoagaricus serenus* and *L. crystallifer* are further distinguished by their ovoid and broadly amygdaliform

Table 1. *Leucoagaricus* species and specimens, and *Lepiota subgracilis* outgroup, used for ITS phylogenetic analyses.

Species	Voucher	Country	GenBank no.
L. americanus	Vellinga 2454 (UCB)	USA	AY176407
	JRH091509-1 (TENN)	USA	MF773593
L. asiaticus	LAH5872011	Pakistan	KP164972
	LAH10012012	Pakistan	KP164971
L. badius	LAH SH210	Pakistan	KU647734
	LAH SH148	Pakistan	KU647736
L. bresadolae	Bas7981	USA	AF295929
	MCVE:756	Italy	GQ329047
	CCBAS802	Czech Rep.	LN714565
L. brunneus	LAH35862 [T]	Pakistan	MH990662
L. crystallifer	Huijser (L)	Germany	AF482863
	SFC 1010003-02	Spain	KY350216
L. dyscritus	Vellinga 3532B (UC)	USA	GU136181
	Vellinga 3956 (UC)	USA	GU136180
L. gaillardii	MCVE:16517	Italy	GQ329064
	MCVE:736	Italy	GQ329042
L. griseodiscus	MCVE:13719	Italy	GQ329059
L. japonicus	J. Li 221	China	KY039572
L. jubilaei	Guinberteau 99101101	France	AY243635
	10115A	USA	KX258658
L. lacrymans	Zhang 599	China	KY039574
L. lahorensiformis	FH-SHL2	Pakistan	KU647730
	LAH SHL2	Pakistan	KU647729
L. littoralis	MCVE:856	Italy	GQ329051
	MCVE:702	Italy	GQ329041
	MCVE:13721	Italy	GQ329060
L. cf. *majusculus*	MFLU 09-0164	Thailand	HM488764
L. medioflavoides	MCVE:2324	Italy	GQ329055
L. meleagris	IMG 1671	USA	KY680786
	Vellinga 2095 (L)	Netherlands	AF482867
	Vellinga 1990 (L)	Netherlands	AY176419
	CAW-9	India	GQ249888

L. menieri	herb. Huijser	Netherlands	KP300879
L. nivalis	Yang 5792	China	KY039573
L. pakistaniensis	LAH SJF13	Pakistan	KU647727
	LAH SJF23	Pakistan	KU647728
L. purpureolilacinus	MCVE:754	Italy	GQ329045
	Vellinga 2291 (L)	Netherlands	AF482869
L. rubroconfusus	ZT13003 (ZT)	USA	KP300875
L. rubrotinctus	gr0557	China	KP300877
	gr157	China	KP300876
	KUN:HKAS 54317	China	JN944082
	KUN:HKAS 54240	China	JN944081
	—	China	JX827166
L. sardous	AC5195	Spain	KT992149
Leucoagaricus sp.	Thiele 2646	Australia	AY176432
	JZB2115002	China	JN907015
	BAB 4737	India	KR154966
	Ge 97	China	KP096237
	Yang 3972	China	KP096238
	Vellinga 2561	USA	AY176430
	TENN:070790	USA	MF686514
	FLAS-F-60259	USA	MF153051
	M.M. Rogers (UCB)	USA	AY176434
	Vellinga 2484 (UC)	USA	GU136182
L. subcrystallifer	Ge 878	China	KP096236
L. sublittoralis	Ecv2235	Netherlands	AY176442
L. subpurpureolilacinus	Yang 3959	China	KP096234
	Ge 406	China	KP096233
L. subvolvatus	Brand s.n. (L)	USA	KP300878
L. sultanii	LAH SH115b	Pakistan	KU647732
	LAH SH115	Pakistan	KU647733
L. truncatus	Ge 793	China	KP096235
L. umbonatus	LAH SHL1	Pakistan	KU647737
	LAH SHL8	Pakistan	KU647738
L. vassiljevae	LE 10350	Russia	JX133169
	LE 289338	Russia	JX133170
	LE 289432	Russia	JX896447
L. viscidulus	AC4187	Spain	KT992148
L. volvatus	AC1785	Spain	KT992150
Lepiota subgracilis	Vellinga 1783 (L)	Netherlands	AY176490
	HKAS 5802	China	EU416290

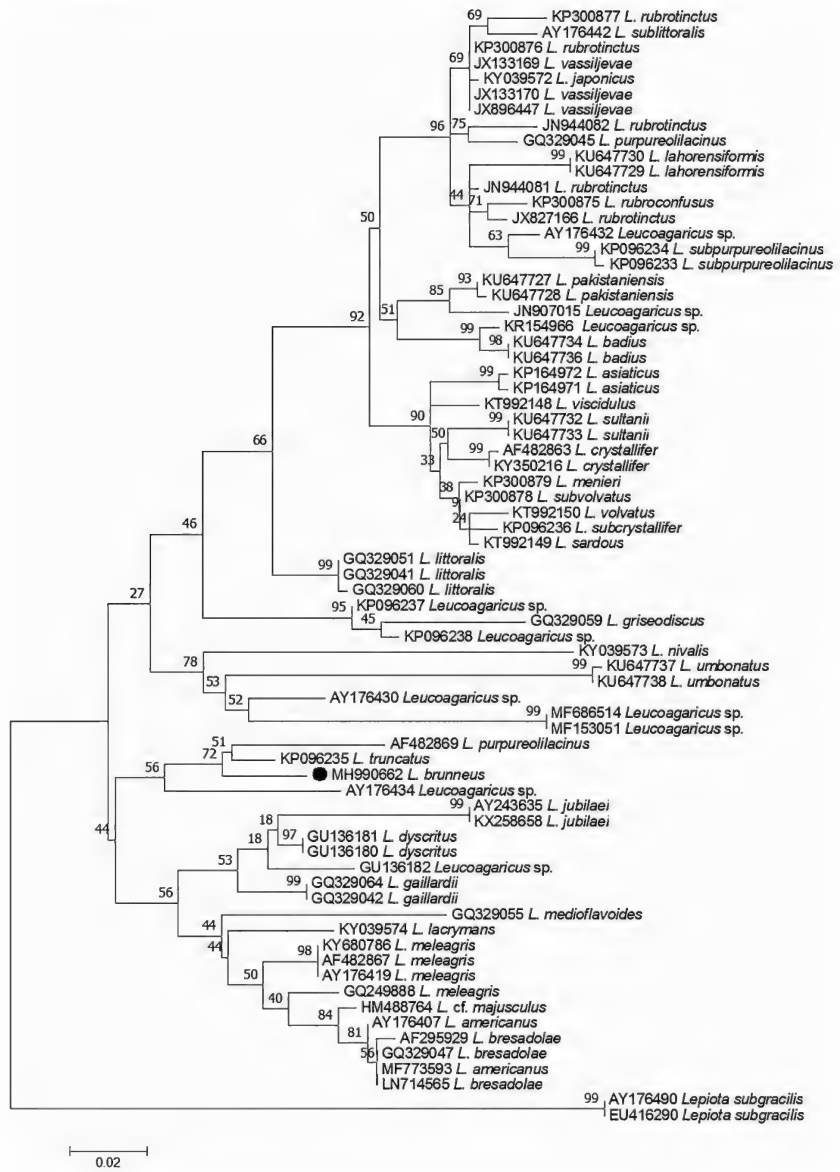

FIGURE. 3. Molecular phylogenetic analysis of ITS sequences of *Leucoagaricus* species, with *Lepiota subgracilis* outgroup. The evolutionary history was inferred by using the Maximum Likelihood method based on the Tamura 3-parameter model. The analysis involved 72 nucleotide sequences. All positions containing gaps and missing data were eliminated. There were a total of 448 positions in the final dataset. Our new species is marked with ●.

basidiospores, contrasting with the elongated to cylindric and amygdaliform basidiospores of *L. brunneus.* In addition, in *L. crystallifer* the cheilocystidia have obvious crystals on the surface (Vellinga 2000, 2001) unlike the smooth cheilocystidia of *L. brunneus.*

In comparison with Pakistani *Leucoagaricus* species, *L. brunneus* differs from *L. asiaticus* characterized by oblong to ellipsoid spores and cheilocystidia with crystals at the apex (Ge & al. 2015). Morphologically, its pileus color distinguishes *L. brunneus* (brown) from *L. badius* (red), *L. pakistaniensis* (whitish), *L. lahorensis* (dark reddish brown), *L. lahorensiformis* (light orange), *L. umbonatus* (yellowish pink), and *L. sultanii* (dark yellow) (Qasim & al. 2015, Hussain & al. 2018). Basidiospore morphology also separates these species from *L. brunneus* (Qasim & al. 2015, Hussain & al. 2018). All the earlier named Pakistani species have smaller spores except *L. lahorensis,* whose spores measure more or less the same as *L. brunneus* (Qasim & al. 2015), and none except *L. brunneus* present the same basidiospore shape—elongate to cylindrical in face view and amygdaliform in profile: amygdaliform to oblong in *L. badius* (6.5–7.5 × 4–5 µm), ellipsoid to rarely amygdaliform in *L. pakistaniensis* (7.5–8 × 4.5–5 µm), broadly ellipsoid to ellipsoid in *L. lahorensis* (8–10.6 × 6.4–7.6 µm), fusiform to amygdaliform in *L. lahorensiformis* (6.5–7.5 × 3.5–4 µm), amygdaliform to ellipsoid in *L. umbonatus* (5.5–6.5 × 3.5–4 µm), and amygdaliform to ellipsoid in *L. sultanii* (5.5–7 × 3.5–4.5 µm) (Qasim & al. 2015, Hussain & al. 2018). The crystals on the cheilocystidial apices in *L. lahorensiformis* and *L. sultanii* also separate both species from *L. brunneus.*

Therefore a combination of morphological differences and a phylogenetic bootstrap support of 72% (Fig. 3) provide convincing support for our new species, *Leucoagaricus brunneus.*

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Dictyostelids from Jilin Province, China 3: new *Cavenderia* and *Dictyostelium* records

Pu Liu[1], Shunhang Zhang[1], Yue Zou[1], Xueping Kang[2], Yu Li[1*]

[1] *Engineering Research Center of Chinese Ministry of Education for Edible and Medicinal Fungi, Jilin Agricultural University, Changchun, 130118, P. R. China*

[2] *Yanbian Academy of Agricultural Sciences, Yanji 133001, P. R. China*

* Correspondence to: *fungi966@126.com*

Abstract—*Cavenderia parvispora, Dictyostelium vermiforme,* and *D. dimigraforme,* isolated from samples of soil collected in Jilin Province, China, represent new records from China. Descriptions and illustrations based on these isolates are provided.

Key words—*Cavenderiaceae,* cellular slime molds, *Dictyosteliaceae, Mycetozoa,* taxonomy

Introduction

Dictyostelid cellular slime molds (dictyostelids), with both animal-like (protozoan) and fungus-like characteristics, are primarily inhabitants of the soil and leaf litter/humus zone of fields and forests, along with animal dung, where they feed mostly on bacteria. These organisms play an essential role in maintaining the balance that exists between bacteria and other soil organisms (Singh 1947; Cavender & Raper 1965a,b; Raper 1973, 1984). Traditional morphological classifications distributed dictyostelids among four genera based on differences in sorophore structure and branching patterns (Kirk & al. 2008). However, a new classification based on unique 18S rRNA sequence signatures was proposed by Sheikh & al. (2018).

Jilin Province is situated in the temperate zone of China and is characterized by a monsoon climate (Liu & Li 2014). Previously, a total of 15 species, including two new dictyostelid species, have been reported from Jilin Province (He & Li

2008; Liu & Li 2014, 2017). We report another three species in *Cavenderia* and *Dictyostelium* for the first time from China.

Materials & methods

Sampling, isolation, cultivation—Samples of soil were collected from three localities in Jilin Province in 2008 and 2009. Each 10–20 g soil sample was placed in a sterile whirl-pack plastic bag for isolation according to Cavender & Raper (1965a). Each sample was weighed and enough ddH_2O added for an initial dilution of 1:10. A 0.5 mL aliquot of this dilution was added to each of five duplicate culture plates prepared with hay infusion agar (Raper 1984). After c. 0.4 mL of a heavy suspension of the bacterium *Escherichia coli* was added to each culture plate, the plates were incubated at 23 °C with a 12 h light : 12 h dark cycle. Each plate was examined at least once daily for two weeks after the appearance of initial aggregations. Each isolate recovered from one of the plates was purified and cultivated for taxonomic studies. Spores from these isolates were frozen in HL 5 media (Cocucci & Sussman 1970) and stored at –80 °C in the herbarium of the Mycological Institute of Jilin Agricultural University, Changchun, China (HMJAU).

Observation—The isolates were identified using morphological descriptions (Raper 1984) and molecular characteristics (Sheikh & al. 2018). After we marked the location of each early aggregating clone and sorocarp in a plate, we observed life cycle stages under a Zeiss Axio Zoom V16 dissecting microscope with a 1.5× objective and a 10× ocular. Sorocarps were mounted in water on slides for observation and measurements of spores, sorophores, and sorocarps using a Zeiss Axio Imager A2 light microscope mounted with 10× ocular and 10, 40, and 100× (oil) objectives. Photographs were taken with Zeiss Axiocam 506 color microscope camera.

Taxonomy

Cavenderia parvispora (H. Hagiw.) S. Baldauf, S. Sheikh & Thulin, Protist 169(1): 20. 2018. Plate 1a–d

When cultured at 23 °C on non-nutrient agar with *E. coli*, sorocarps gregarious or solitary, unbranched or sparsely irregularly branched, sometimes prostrate, phototropic, normally 0.2–4.4 mm long. Sorophore colorless, sinuose, slender, tapering from bases to tips, consisting of one tier of cells except for the in base and tip, bases clavate, tips clavate. Sori white, globose, commonly 30–150 μm diam. Spores hyaline, elliptical, 3.7–6.0 × 1.9–2.9 μm, with a few conspicuous polar granules. Aggregations with radiate streams or mound-like.

Specimen examined: **China, Jilin Province**, Zuojia, isolated from soil (S0425) from a broadleaf forest, 9 Sep. 2008 (HMJAU MR056).

Comments: *Cavenderia parvispora* was first isolated from forest soil sampled in Japan (Hagiwara 1989). Its medium-sized sorocarps, thin delicate sorophores with clavate tips, and small elliptical spores readily distinguish this species from morphologically similar dictyostelids.

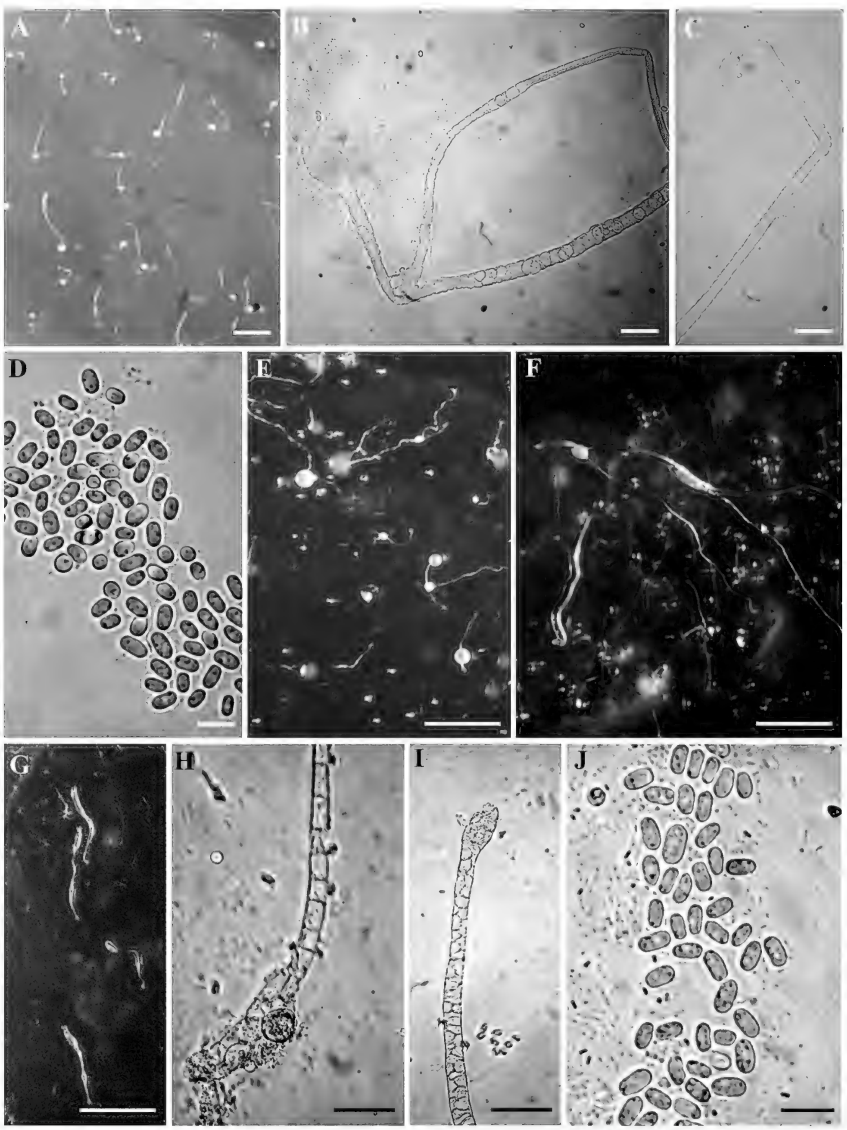

Plate 1. ***Cavenderia parvispora*** (HMJAU MR056): A. Sorocarps; B. Sorophore base; C. Sorophore tip; D. Spores. ***Dictyostelium vermiforme*** (HMJAU MR058): E. Sorocarps; F, G. Vermiform and curved sorogens; H. Sorophore base; I. Sorophore tip; J. Spores. Scale bars: A, E = 2 mm; B, C, H, I = 5 μm; D, J = 10 μm; F, G = 1 μm.

Dictyostelium vermiforme Vadell & Cavender, Mycologia 99: 118. 2007. PLATE 1E–J

When cultured at 23 °C on non-nutrient agar with *Escherichia coli*, sorocarps clustered or solitary, normally prostrate, 1.0–2.0 mm long. Sorophore colorless, tapering from bases to tips, consisting of one tier of cells except for the base and tip, bases small round or expanded, tips capitate or expanded. Sori white, globose, commonly 50–130 μm diam. Spores hyaline, oblong to elliptical, 4.7–7.0 × 2.9–3.9 μm, with sparse or prominent polar granules. Aggregations with flattened streams, forming mound-like early sorogens. Sorogens developing rapidly, becoming vermiform and curved, migrating freely to form sinuous and curled late sorogens with prostrate sorophores.

SPECIMEN EXAMINED: **CHINA, JILIN PROVINCE**, National Nature Reserve, isolated from soil (S0083-1) from a broadleaf forest, 10 Jun. 2009 (HMJAU MR058).

COMMENTS: *Dictyostelium vermiforme* was originally isolated from soil/litter sampled in Iguazú Regional Park, Argentina (Vadell & Cavender 2007). This species is characterized by its vermiform and curved early migrating sorogens.

Dictyostelium dimigraforme Cavender, J. Gen. Microbiol. 62: 115. 1970. PLATE 2

When cultured at 23 °C on non-nutrient agar with *Escherichia coli*, sorocarps normally solitary, unbranched, erect or inclined, 3.5–10.5 mm long. Sorophore colorless or slightly yellow, tapering from bases to tips, consisting of one tier of cells except for the base and tip, bases round or slightly enlarged, tips capitate. Sori globose, off-white to yellow, 220–380 μm diam. Spores hyaline, oblong to elliptical, 7.7–12.0 × 2.9–4.9 μm, without polar granules. Aggregations radiating.

SPECIMEN EXAMINED: **CHINA, JILIN PROVINCE**, Chanchung, Jingyuetan National Natural Park, isolated from soil (S0446) from a broadleaf forest, 10 Sep. 2008 (HMJAU MR059).

COMMENTS: *Dictyostelium dimigraforme* was isolated the first time from surface soil sampled in a tropical forest in the West Indies (Raper 1984). This species is characterized by its yellow sori and round bases, and can be distinguished from *D. discoideum* by its lack of basal disk.

Discussion

Our study has raised to 18 the number of dictyostelid species known from Jilin Province. Jilin Province is located in the temperate zone which has rich forests optimal for dictyostelids. The three dictyostelid species (*Cavenderia parvispora, Dictyostelium vermiforme,* and *D. dimigraforme*) reported here do not appear to be distributed worldwide (Hagiwara 1989, Vadell & Cavender 2007, Raper 1984). In particular, *Dictyostelium vermiforme* (originally isolated

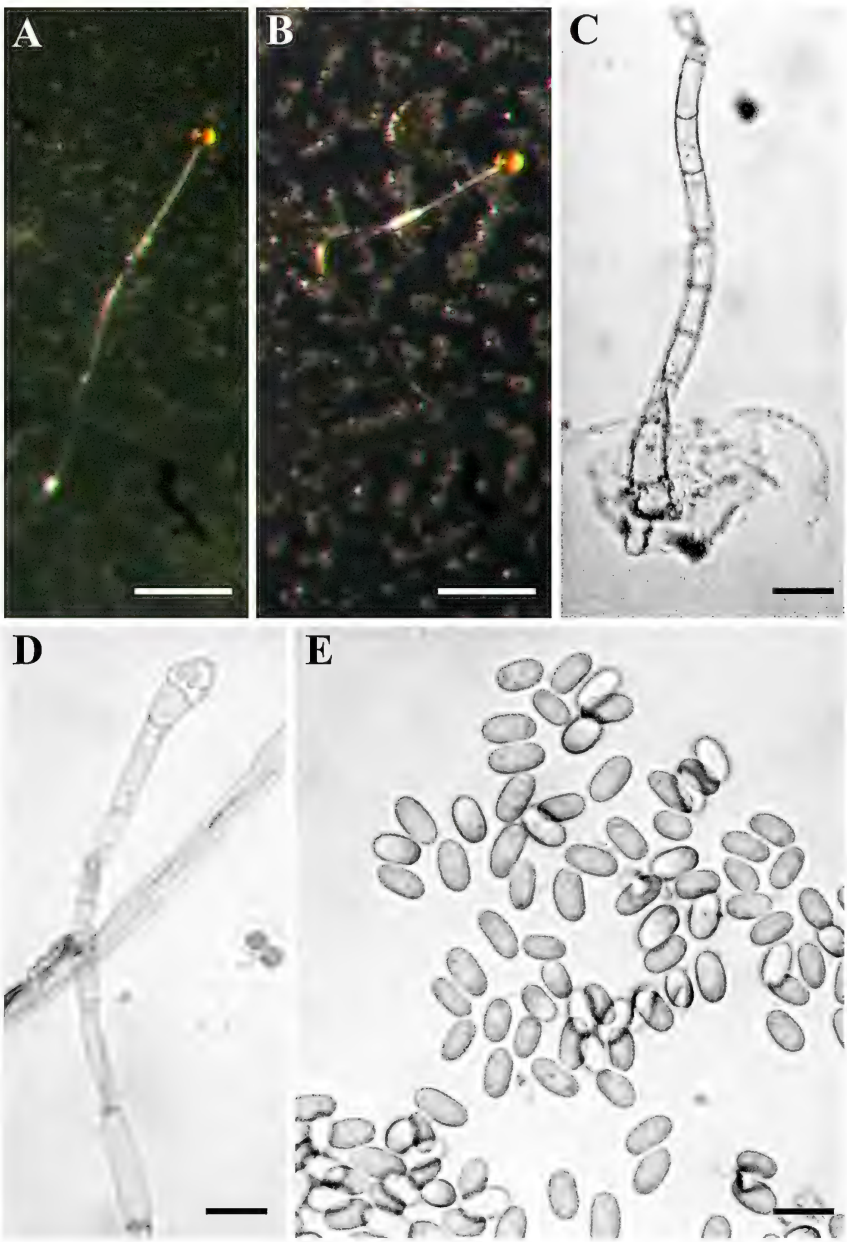

Plate 2. ***Dictyostelium dimigraforme*** (HMJAU MR059): A, B. Sorocarps; C. Sorophore base; D. Sorophore tip; E. Spores. Scale bars: A, B = 2 mm; C, D = 5 μm; E = 10 μm.

from c. 26°S in South America) and *D. dimigraforme* (originally isolated from c. 11°N in the West Indies) have now been isolated from c. 44°N in Asia. Clearly, the dictyostelids of Jilin Province need to be investigated in more detail.

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Records of *Aureobasidium harposporum*, *Sarcophoma miribelii*, and *Stigmina dothideoides* from Turkey

Makbule Erdoğdu[1*], Merve Ulukapı[2], Ali Ihsan Karayel[2], Zekiye Suludere[3]

[1] *Department of Landscape Architects, Faculty of Agriculture &*
[2] *Graduate School of Natural and Applied Sciences: Ahi Evran University, Bağbaşı, Kırşehir, Turkey*
[3] *Department of Biology, Faculty of Science, Gazi University, Teknikokullar, Ankara, Turkey*

* Correspondence to: *merdogdu@ahievran.edu.tr*

Abstract—During field studies on the microfungi in Mucur District of Kırşehir Province, *Aureobasidium harposporum*, and *Stigmina dothideoides* were revealed as new records for Turkey; and *Sarcophoma miribelii*, previously recorded from northeastern Turkey, is reported from central Turkey. Distinguishing morphological characters of these species are described, and their photographs are provided.

Key words—*Ascomycota*, *Dothideales*, leaf pathogenic fungi, *Mycosphaerellales*, SEM

Introduction

Aureobasidium Viala & G. Boyer (*Saccotheciaceae*, *Dothideales*) contains 24 species (Index Fungorum 2018). The genus is characterized by synchronous conidium production on hyaline conidiogenous cells. Species of *Aureobasidium* produce variously shaped one-celled conidia from terminal, lateral, or intercalary hyaline conidiogenous cells. Members of this genus occur as saprophytes on a variety of substrates or as parasites on phanerogams (Hermanides-Nijhof 1977).

Sarcophoma Höhn. (*Dothioraceae, Dothideales*) was proposed by Höhnel in 1906 as a monotypic genus, but four species are now accepted (Index Fungorum 2018).

Stigmina Sacc. (*Mycosphaerellaceae*, *Mycosphaerellales*) was established by Saccardo in 1880; c. 80 species are currently accepted in the genus (Index Fungorum 2018). In Turkey, the *Stigmina* species are poorly known and have not yet been intensively studied; of the four species reported from Turkey—*S. carpophila*, *S. compacta*, *S. obtecta*, *S. platani*—(Göbelez 1964, Hüseyin & al. 2003, Çimen & Ertuğrul 2007, Erdoğdu & Hüseyin 2008), two have been transferred to other genera: *S. compacta* [≡ *Thyrostroma compactum*] and *S. platani* [≡ *Pseudocercospora platanigena*].

Materials & methods

Host specimens were prepared following conventional herbarium techniques. Host plants were identified using the Flora of Turkey and East Aegean Islands (Davis 1965–85). Thin fungal sections prepared from host tissue were examined under a Leica DM E light microscope and measured from mounts in tap water. Infected host surfaces were photographed using a Leica EZ4D stereomicroscope. The fungi were identified using relevant literature (for *Aureobasidium*: Saccardo 1892 (as *Gloeosporium*), Hermanides-Nijhof 1977; for *Sarcophoma*: Saccardo 1884 (under *Phoma*), Morgan-Jones 1971, Aa 1975; for *Stigmina*: Ellis 1959, Shoemaker & Egger 1982). All examined specimens were deposited in the Mycology Laboratory of Ahi Evran University, Department of Biology, Kırşehir, Turkey (AEUT).

For scanning electron microscopy (SEM), 8–10 mm square pieces of infected leaf were mounted on aluminium stubs with double-sided adhesive tape. They were coated with gold using Polaron SC 502 Sputter Coater and were examined with Jeol JSM 6060 scanning electron microscope operated at 5–10 kV in the Electron Microscopy Unit, Faculty of Science, Gazi University, Ankara, Turkey.

Taxonomy

Aureobasidium harposporum (Bres. & Sacc.) Herm.-Nijh., Stud. Mycol. 15: 151 (1977) PLATE 1

SPOTS visible on both sides of leaves and twigs, generally leaves beginning to dry from the tip, brown on the upper surface, fuscous chestnut on the lower surface, spots margin dark brown; infected leaves dropping prematurely from the shrub. CONIDIOMATA acervular, subepidermal, yellowish, broadly elliptical, 196–330 µm diam. CONIDIOGENOUS CELLS erect, densely packed, clavate to subcylindrical, 10–20 × 3.5–6.5 µm, forming conidia simultaneously at the apex. CONIDIA one-celled, falcate, sometimes elliptical or slightly curved, oil droplet, smooth-walled, 13.7–19.3(–21.8) × 4.4–5.4 µm, hyaline.

SPECIMEN EXAMINED—**TURKEY, KIRŞEHIR, Mucur District**, Tekken Village, 39°02′13″N, 34°13′08″E, 977 m asl, on living leaves and stems of *Viscum album* L. subsp. *album* (*Santalaceae*), 19.06.2013, M. Ulukapı (AEUT MU1050).

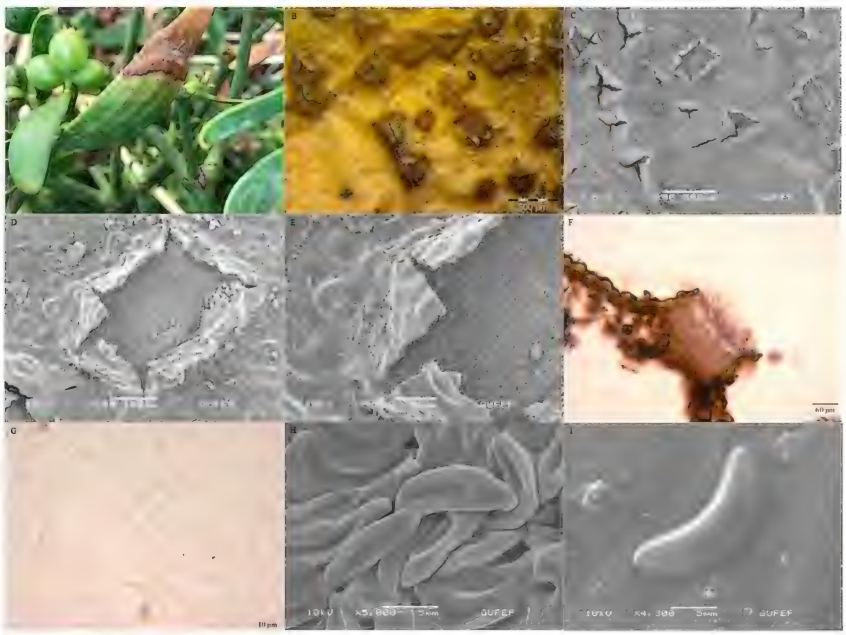


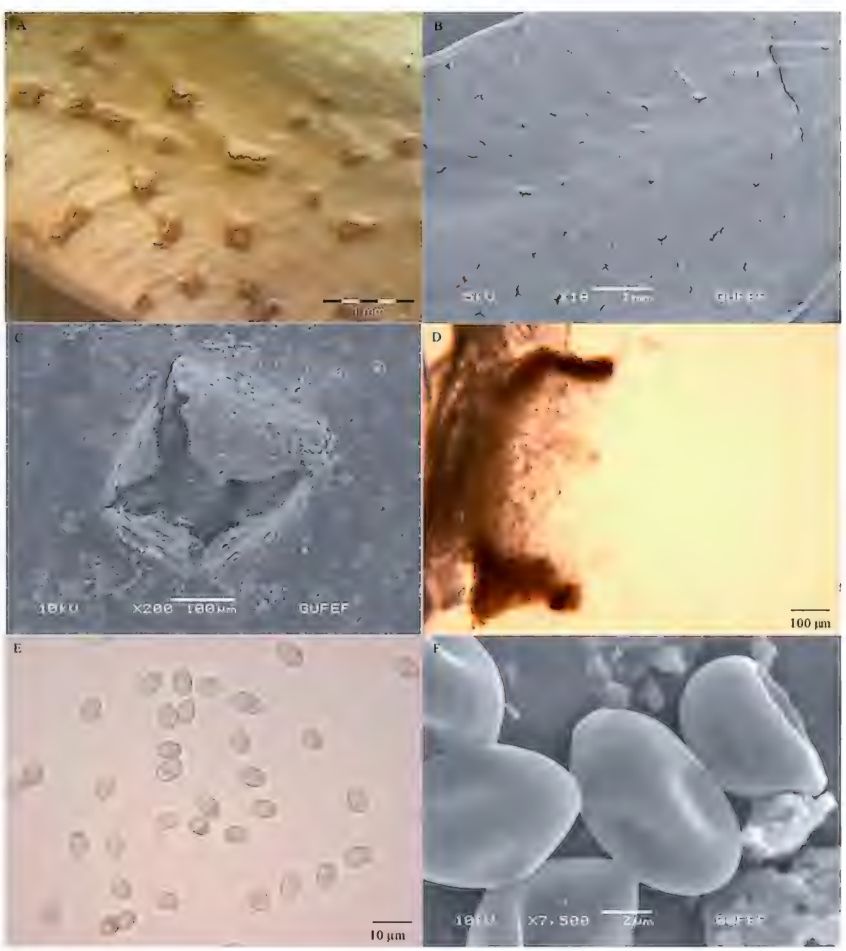
Plate 1. *Aureobasidium harposporum* (AEUT MU1050). A. leaf spots; B. acervuli on leaf; C. acervuli on leaf (SEM); D, E. acervulus on leaf (SEM); F. acervulus, vertical section; G. conidia; H, I. conidia (SEM).

Notes: *Viscum album* (European mistletoe) is an evergreen, perennial, epiphytic, hemiparasitic shrub that lives on a wide range of woody plant species (Zuber 2004). European mistletoes can affect their host trees in many ways. Known effects from mistletoe infection include lowering the vigor of the host, inducing premature mortality, reducing quality and quantity of wood grown, reducing fruit production, and predisposing trees to secondary infection by other agents, such as insects or decay fungi (Hawksworth 1983).

Biological control of parasites by using plant pathogens has gained acceptance as a practical, safe, and environmentally beneficial management method applicable to agro-ecosystems (Charudattan 2001). The use of biological control agents for weed control has attracted increased attention (Özaslan & al. 2013; Özaslan 2016), and diagnosing host weeds and their natural enemies is the foundation stone of a successful biological control program (Özaslan 2016). Control of European mistletoe is an important consideration for the forest service in Turkey (Yüksel & al. 2005). Over 20 microscopic fungi live on European mistletoe, but only a few of them cause major damage to the plant

(Karadžić & al. 2004). Of these, *Aureobasidium harposporum*, which causes leaf spot disease of European mistletoe, appears to have potential as a biological control agent against of this semi-parasite. In this study, *Aureobasidium harposporum* on living leaves and stems of *Viscum album* subsp. *album* is reported as new to the mycobiota of Turkey.

The Turkish specimen agrees with other reports of *Aureobasidium harposporum* in conidiomata and conidia morphology, the only observable difference being the smaller dimensions of acervuli and conidia. Saccardo (1892) describes 200 µm diam. acervuli and 18–20 × 4–5 µm conidia, while Hermanides-Nijhof (1977) cites 250–500 µm acervuli and (16–)17–21(–23) × 3.5–5 µm conidia.



Sarcophoma miribelii (Fr.) Höhn., Hedwigia 60: 133 (1918) PLATE 2

≡ *Macrophoma miribelii* (Fr.) Berl. & Voglino, Atti Soc. Veneto-Trent. Sci. Nat.10(1): 179 (1886)

PYCNIDIA numerous, hypophyllous (rarely epiphyllous), at first covered by the epidermis, later becoming erumpent, scattered, 143–289 µm diam., yellowish or brown. CONIDIA single-celled, ovoid, rounded at apex, attenuate at the base, smooth-walled, (8.4–)10–13.6(–14.3) × 6.2–8.7 µm, hyaline, with granular contents.

SPECIMEN EXAMINED—**TURKEY, KIRŞEHIR, Mucur District**, Seyfegölü, 39°06′58″N, 34°12′11″E, 1135 m asl, on living leaves and stems of *Buxus sempervirens* L. (*Buxaceae*), 16.04.2014, M. Ulukapi (AEUT MU1099).

NOTES: Our Turkish specimen is morphologically similar to *Sarcophoma miribelii* specimens described in the literature (Saccardo 1884, Morgan-Jones 1971, Aa 1975). *Sarcophoma miribelii* has previously been reported (without description or illustration) from Rize Province in coastal northeastern Turkey (Göbelez 1964, Hüseyin & al. 2005; both as *Macrophoma mirbelii* [sic]), whereas our new record is from Kırşehir Province in central Turkey at c. 1100 m asl. *Sarcophoma miribelii* is found worldwide, wherever the *Buxus* host occurs (Aa 1975).

Stigmina dothideoides (Ellis & Everh.) M.B. Ellis, Mycol. Pap. 72: 53 (1959) PLATE 3

SPORODOCHIA erumpent through epidermis, pustulate, 1–4 mm diam., circular to elliptical, blackish. CONIDIOPHORES densely crowded, arising from stromatic hyphae, pale brown to medium brown, cylindrical to lageniform, 1–2- septate, often branched at the base. CONIDIA blastic, solitary and terminal, elliptical to obovoid, at first one-celled, becoming 3–septate, non-constricted or slightly constricted at the septum, rounded at apex, truncated to obtusely rounded at the base, smooth-walled, 25–38 × 11.8–13.9(–14.5) µm, golden brown.

SPECIMEN EXAMINED—**TURKEY, KIRŞEHIR, Mucur District**, Gümüşkümbet Village, 39°05′52″N, 34°12′26″E, 1180 m asl, on stems of *Artemisia* sp. (*Asteraceae*), 16.04.2014, M. Ulukapı (AEUT MU1087).

NOTES: The species was first described by Ellis & Everhart (1891, as *Clasterosporium dothideoides*), who observed symptoms on stems of *Artemisia cana* and *Shepherdia argentea* in Montana, USA; and it has

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PLATE 2 (left). *Sarcophoma miribelii* (AEUT MU1099). A. pycnidia on leaf; B. pycnidia on leaf (SEM); C. pycnidium on leaf (SEM); D. pycnidium, vertical section; E. conidia; F. conidia (SEM).

Plate 3. *Stigmina dothideoides* (AEUT MU1087). Top left. conidia and conidiophores; Top right. conidium and conidiophore; Bottom. conidia.

been recorded on *Gaillardia aristata* further north in Alberta, Canada (Shoemaker & Egger 1982). *Stigmina dothideoides* on branches of *Artemisia* sp. is reported as new to the mycobiota of Turkey.

Although our Turkish specimen of *Stigmina dothideoides* is morphologically similar to specimens described in the literature, it differs slightly in having shorter and narrower 3-septate conidia, compared with 25–46 × 13–19 µm 3-septate conidia in Ellis (1959) and 30–38(–42) × (12.3–)14–16.8 µm 3(–4)-septate conidia in Shoemaker & Egger (1982).

Acknowledgments

The authors thank Sevda Kirbağ (Department of Biology, Fırat University, Elazığ, Turkey) and Cumali Özaslan (Department of Plant Protection, Dicle University, Diyarbakir, Turkey) for pre-submission review. This work was supported by the Ahi Evran University Scientific Research Projects Coordination Unit. (Project Number: PYO-Fen.4003.13.005 and FEF.A4.17.006).

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Bactrodesmium pulcherrimum sp. nov. from Ecuador

Fernando Espinoza[1], Daynet Sosa[1*], Lizette Serrano[1], Adela Quevedo[1], Freddy Magdama[1], Marcos Vera[1], Simón Pérez-Martinez[2], Elaine Malosso[3], Rafael F. Castañeda-Ruiz[4]

[1] *Escuela Superior Politécnica del Litoral, ESPOL, (CIBE), Campus Gustavo Galindo Km. 30.5 Vía Perimetral, P.O. Box 09-01-5863, Guayaquil, Ecuador*

[2] *Universidad Estatal de Milagro (UNEMI), Facultad de Ingenieria, Cdla. Universitaria Km. 1.5 vía Milagro-Km26. Milagro 091706, Guayas, Ecuador*

[3] *Centro de Biociências, Departamento de Micológica, Universidade Federal de Pernambuco, Avenida da Engenharia, s/n Cidade Universitária, Recife, PE, 50.740-600, Brazil*

[4] *Instituto de Investigaciones Fundamentales en Agricultura (INIFAT), Tropical 'Alejandro de Humboldt', OSDE, Grupo Agrícola, Calle 1 Esq. 2, Santiago de Las Vegas, C. Habana, Cuba, C.P. 17200*

* Correspondence to: *dasosa@espol.edu.ec*

Abstract—A new species *Bactrodesmium pulcherrimum*, found on decaying wood in Ecuador, is described and illustrated. The fungus is distinguished by subnapiform to broadly subturbinate (maize kernel-shaped) 1-septate asymmetrical ochreous-brown conidia. Illustrations of *Bactrodesmium novageronense* and *B. simile* and a comparison table of bicellular *Bactrodesmium* species are also provided.

Key words—asexual fungi, freshwater, hyphomycetes, taxonomy, tropics

Introduction

Saprobic dematiaceous hyphomycetes are highly diverse on plant materials in Central and South American tropical forests, where many new genera and species have recently been discovered (Castañeda-Ruiz &

Fig. 1. Cacao plantation, Guayas Province, Ecuador.

al. 2016). During a survey of hyphomycetes associated with plant debris of cacao plantations in the Naranjal, Guayas province, southern Ecuador (Fig. 1), we collected a *Bactrodesmium* specimen that differs remarkably from all previously described species (Hernández-Restrepo & al. 2013, Arias & al. 2016). It is described here as a new species, *Bactrodesmium pulcherrimum*.

Materials & methods

Samples of decaying plant materials were collected and placed in plastic bags for transport to the laboratory, where they were washed, treated according to Castañeda-Ruiz & al. (2016), and placed in humid chambers. Several attempts to obtain this species in pure culture were unsuccessful after using a flamed needle to transfer conidia to corn meal agar mixed 1:1 with carrot extract and incubating at 25 °C. Mounts were prepared in PVL (polyvinyl alcohol, lactic acid) and measurements were made at 1000× magnification. Microphotographs were obtained with an Olympus BX51 microscope equipped with bright field and Nomarski interference optics. The type specimen is deposited in the Herbarium of Universidade Federal de Pernambuco, Recife, Brazil (URM).

Taxonomy

Bactrodesmium pulcherrimum R.F. Castañeda, F. Espinoza & D. Sosa, **sp. nov.** Fig. 2

MB 830569

Differs from *Bactrodesmium simile* by its hemispherical conidial basal cells and maize kernel-shaped conidia.

Type: Ecuador, Guayas Province, Guayaquil, Naranjal, 02°41′26″S 79°36′46″W, on decaying wood of *Theobroma cacao* L. (*Malvaceae*), 7 March 2018, F. Espinoza & M. Vera (**Holotype**, URM 91287).

Etymology: Latin, *pulcherrimum*, meaning most beautiful.

Conidiomata on the natural substrate sporodochial, scattered, pulvinate ochreous to brown, ≤20 µm diam. Mycelium superficial and immersed composed of septate, branched, hyaline, smooth hyphae, 2–3 µm diam. Conidiophores macronematous, mononematous, unbranched or with short lateral branches scorpioid after 1–2 sympodial elongations of the conidiogenous cells, erect, flexuous, 2–3-septate, hyaline, smooth, 30–80 × 4–5 µm. Conidiogenous cells monoblastic, integrated or discrete, cylindrical or slightly clavate, sometimes inflated near the conidiogenous loci, determinate or indeterminate with sympodial extensions, hyaline, 10–18 × 4–7 µm. Conidial secession rhexolytic. Conidia solitary, acrogenous, sometimes acropleurogenous, broadly obovoid to subnapiform, 1-septate, ochreous-brown, smooth, 18–24 ×

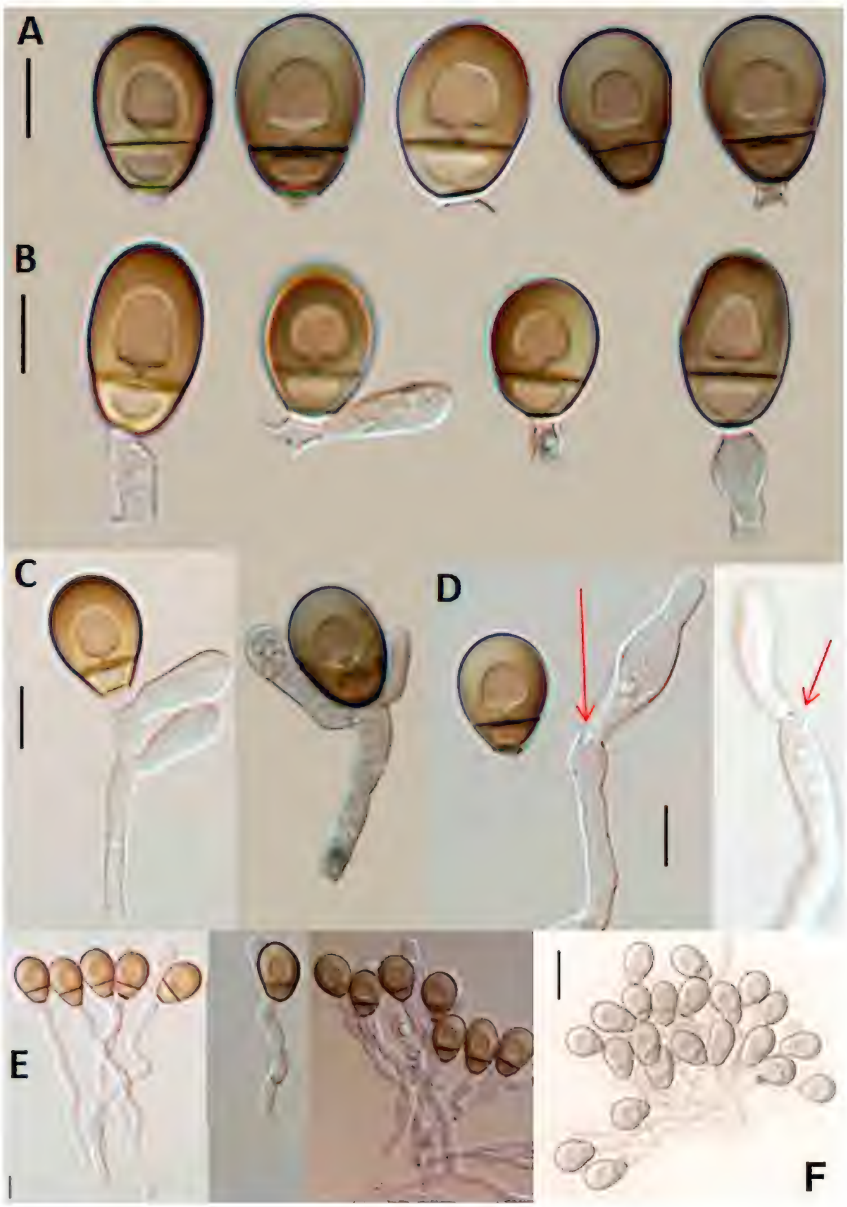

Fig. 2. *Bactrodesmium pulcherrimum* (holotype, URM 91287): A, B. Conidia with a basal frill after rhexolytic conidial secession and a detached conidium with a lateral extension of the conidiogenous cell; C. Conidiogenous cells with lateral sympodial extensions, attached conidia; D. Detached conidium and conidiogenous loci indicated by arrows; E. Conidiophores, conidiogenous cells, and conidia; F. Sporodochium. Scale bars: A–E = 10 µm; F = 20 µm.

13–19 µm, asymmetrical, with a basal cell hemispherical, 5–7 × 10–12 µm, and an apical cell semi-elliptical or subglobose, 12–17 ×13–17 µm, with markedly pale ochreous-brown lumina.

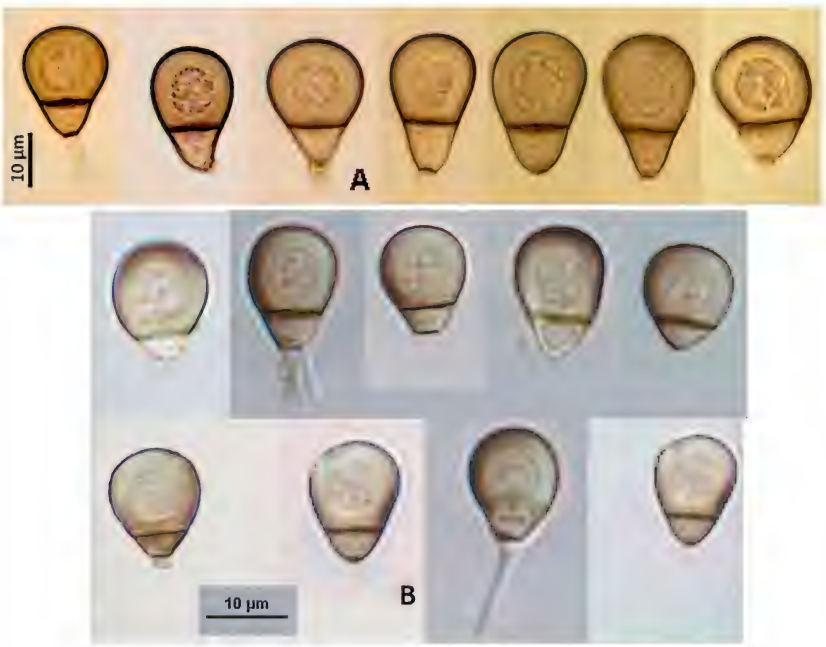

Fig. 3. ***Bactrodesmium simile*** (holotype, XAL CB1689): A. Conidia with a basal frill after rhexolytic conidial secession. ***Bactrodesmium novageronense*** (holotype, INIFAT C84/101-2): B. Conidia with a basal frill after rhexolytic conidial secession. Scale bars = 10 µm.

Note: *Bactrodesmium simile* Arias & al. (Fig. 3A, Table 1) is similar to *B. pulcherrimum* in the conidial sizes, but *B. simile* has broadly pyriform, obovoid, golden brown to pale olivaceous-brown conidia, with a basal

Table 1. Comparison of the 1-septate *Bactrodesmium* species.

Species	Conidial morphology			Reference
	Color	Shape & size (µm)	Basal cell (µm)	
B. novageronense	Pale brown	Obovoid to subglobose 8–13 × 7–10	Hemispherical 3–3.5 × 5–7	Castañeda-Ruiz 1985
B. pulcherrimum	Ochreous-brown	Broadly obovoid to subnapiform 18–24 × 13–19	Hemispherical 5–7 × 10–12	This paper
B. simile	Golden brown to pale olivaceous brown	Broadly pyriform to obovoid 19–24 × 12–16	Cuneiform or obconical 7.5–11 × 5–8.5	Arias & al. 2016

cell cuneiform, 7.5–11 × 5–8.5 µm (Arias & al. 2016). *Bactrodesmium novageronense* R.F. Castañeda (Fig. 3B, Table 1) is similar to *B. pulcherrimum* but can be distinguished by its smaller conidia (8–13 × 7–10 µm; Castañeda-Ruiz 1985).

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Dendrographium multiseptatum sp. nov. from China

Li-Guo Ma, Yue-Li Zhang, Bo Zhang,
Kai Qi, Chang-Song Li, Jun-Shan Qi*

Shandong Key Laboratory of Plant Virology, Institute of Plant Protection, Shandong Academy of Agricultural Sciences, Jinan, Shandong, 250100, China

* Correspondence to: *qi999@163.com*

Abstract—A new species, *Dendrographium multiseptatum*, is described and illustrated from specimens collected on rotten twigs in China. This fungus is characterized by synnematous conidiophores with polytretic conidiogenous cells producing obclavate, 6–9-distoseptate, pale brown conidia.

Key words—asexual morph, microfungi, hyphomycete, taxonomy

Introduction

Dendrographium Massee was established by Massee (1892) to accommodate the Brazilian type species *D. atrum* Massee. The genus is characterized by synnematous, macronematous, unbranched conidiophores with polytretic, integrated, terminal (becoming intercalary), sympodial, cylindrical conidiogenous cells that produce solitary, acropleurogenous, simple, distoseptate conidia (Ellis 1971, Seifert & al. 2011). Species assignment in *Dendrographium* is based primarily on conidial morphology, including shape, septal number, size, pigmentation, and ornamentation. Six additional species have been described (all from India), but *Dendrographium kamatii* V.G. Rao with monotretic conidiogenous cells has been recombined as *Corynespora kamatii* (V.G. Rao) M.B. Ellis (Rao 1963, Ellis 1976). Ghosh & al. (1977) provided a comparison table for the six *Dendrographium* species (including *D. kamatii*) reported from India.

During a survey on wood-inhabiting microfungi in China, a new *Dendrographium* species was found. As this species did not match any of the currently described species in the genus, it is proposed here as new. Specimens are deposited in the Herbarium of Institute of Plant Protection, Shandong Academy of Agricultural Sciences, Jinan, Shandong, China (HSAAS) and the Mycological Herbarium, Institute of Microbiology, Chinese Academy of Sciences, Beijing, China (HMAS).

Taxonomy

Dendrographium multiseptatum L.G. Ma & J.S. Qi, **sp. nov.** FIG. 1

MB 832847

Differs from *Dendrographium atrum* by its narrower conidiophores and its shorter, broader conidia with fewer distosepta and from *D. mitteri* by its longer synnemata, and solitary, shorter, 6–9-distoseptate conidia.

TYPE: China, Shandong Province, Taian City, Taishan District, on rotten twigs of an unidentified plant, 22 May 2018, L.G. Ma (**Holotype**, HSAAS 0415; **isotype**, HMAS 146095).

ETYMOLOGY: *multiseptatum*, referring to the numerous conidial septa.

COLONIES on the natural substratum effuse, black to dark brown, tufted. Mycelium mostly immersed in the substratum. Synnemata large, black, erect, tapered towards the apex, with dark brown stalks, consisting of parallel conidiophores, 520–1380 µm long, 25–85 µm diam. at the base. CONIDIOPHORES macronematous, synnematous, mostly adpressed along lower part of the length, divergent towards the upper part, unbranched, erect, straight or flexuous, cylindrical, septate, dark brown, smooth, thick-walled, brown towards the apex, ≤1400 µm long, 3.5–6.5 µm diam. CONIDIOGENOUS CELLS integrated, terminal becoming intercalary, polytretic, cylindrical, brown, smooth, thick-walled, 8–24 × 5.0–7.5 µm. CONIDIA solitary, acropleurogenous, simple, obclavate, 6–9-distoseptate, smooth, thick-walled, pale brown, 32–66 × 8–11.5 µm, tapered towards the apex, with a basal scar, truncate at the base, 2.5–3.5 µm diam.

COMMENTS—*Dendrographium multiseptatum* most closely resembles *D. atrum* and *D. mitteri* Syd. in conidial shape. However, *D. atrum* has broader (6–10 µm) conidiophores and longer and narrower conidia with more distosepta (40–130 × 7–9 µm, 6–15 distosepta; Massee 1892). *Dendrographium mitteri* differs by its shorter synnemata (170–250 µm) and occasionally catenate, longer (35–110 µm), 3–10-septate conidia (Sydow & Mitter 1933).

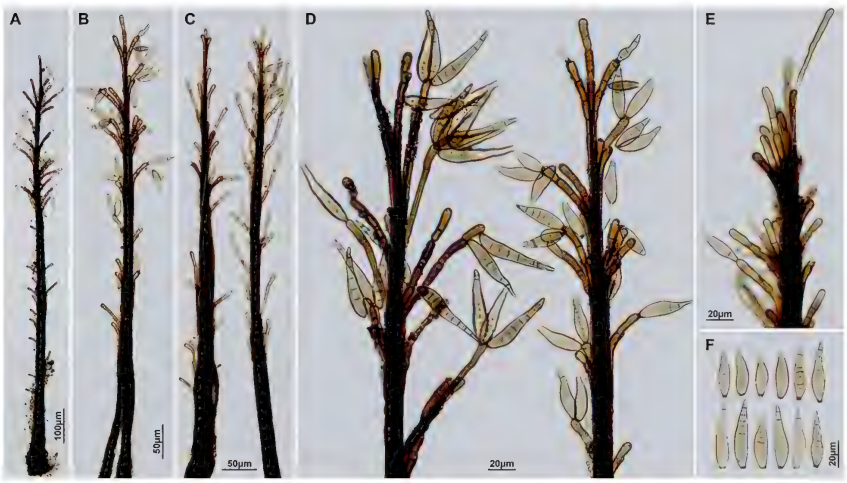

Fig. 1. *Dendrographium multiseptatum* (holotype, HSAAS 0415): A–D. Synnematous conidiophores, conidiogenous cells, and conidia; E. Synnematous conidiophores with conidiogenous cells and conidium; F. Conidia.

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The authors express gratitude to Dr. De-Wei Li (The Connecticut Agricultural Experiment Station Valley Laboratory, Windsor, U.S.A.) and Dr. Ze-Fen Yu (Laboratory for Conservation and Utilization of Bio-resources, Yunnan University, Kunming, P.R. China) for serving as pre-submission reviewers and to Dr. Shaun Pennycook for nomenclatural review. This project was supported by Young Talents Training Program of Shandong Academy of Agricultural Sciences (CXGC2018E04), National Key R & D Program of China (2016YFD0300700, 2017YFD0201700), and National Natural Science Foundation of China (31400019).

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Haematomma pluriseptatum sp. nov. from China

Congcong Miao [#1], Rong Tang [#1,4],
Linlin Dong[2], Zhaojie Ren[3], Zuntian Zhao [*1]

[1] *Key Laboratory of Plant Stress Research, College of Life Sciences &*
[2] *Institute of Environment and Ecology:*
Shandong Normal University, Jinan, 250014, P. R. China
[3] *Shandong Museum, Jinan, 250014, P. R. China*
[4] *The First High School of Liangshan, Shandong Province, 272600, P. R. China*

[*] Correspondence to: *ccmjy123@163.com*

Abstract—A new species, *Haematomma pluriseptatum,* is described from southwestern China. This corticolous species is characterized by large ascospores with (19–)20–26(–27) septa and by the presence of atranorin, russulone, and pseudoplacodiolic acid. A detailed description of its morphology, high resolution photographs, chemistry, comments, and distribution are provided. Related lichen taxa are discussed, and a key to the species of *Haematomma* from China is also provided.

Key words—East Asia, *Haematommataceae*, *Lecanorales*, lichenized fungi, taxonomy

Introduction

The crustose *Haematomma* lichens, with their small but brilliant-red lecanorine apothecia, are often conspicuous on smooth-barked trees in warm-temperate to tropical regions of the world (Staiger & Kalb 1995, Brodo & al. 2008). *Haematomma* was proposed originally to house two species, *H. vulgare* A. Massal. and *H. ventosum* (L.) A. Massal. (Massalongo 1852). The genus is characterized by *Haematomma*-type asci, blood-red lecanorine apothecia, and transversely septate, submuriform to muriform

[#] Congcong Miao & Rong Tang contributed equally to this work.

ascospores (Brodo & al. 2001, Elix 2004, Nelsen & al. 2006, Nash & al. 2004, Smith & al. 2009). Apothecial pigmentation and secondary chemistry play important roles for species delimitation in this genus (Messuti & de la Rosa 2009). The number of spore septa is also used as an important character in separating species (Nelsen & al. 2006). Of the forty *Haematomma* species reported in the world, twelve have been reported in China (Brodo & al. 2001, Elix 2004, Nelsen & al. 2006, Nash & al. 2004, Smith & al. 2009, Tang & al. 2018). For this study, we examined about two hundred specimens of *Haematomma* morphologically and chemically, describe a new species, *H. pluriseptatum*, from China, and present a key to the species of *Haematomma* from China.

Materials & methods

Four collections are deposited in the Lichen Section of the Botanical Herbarium, Shandong Normal University, Jinan, China (SDNU), and one is deposited in the Lichen Herbarium of the Kunming Institute of Botany, Kunming, China (KUN). The specimens were examined morphologically and anatomically morphological under an Olympus SZ51 stereomicroscope and Olympus CX21 polarizing microscope. Both thallus and medulla were tested with K (a 10% KOH aqueous solution) and C (a saturated aqueous NaOCl solution). The lichen substances were identified using standardized thin layer chromatography techniques (TLC) with solvent system A and C (Orange & al. 2010). The specimens were photographed using a DP72 camera on Olympus SZX16 and BX61 microscopes.

Taxonomy

Haematomma pluriseptatum R. Tang, **sp. nov.** Fig. 1

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Differs from *Haematomma rufidulum* by its ascospores with more septa and its production of pseudoplacodiolic acid.

Type: China. Yunnan, Diqing Co., Shangri-La, Tianbao Mt., 27°36′37″N 99°53′37″E, alt. 3790 m, on bark of living trees, 17 Aug. 2018, Wang Chunxiao 20181135 (**Holotype**, SDNU).

Etymology: The epithet *pluriseptatum* refers to the morphology of the ascospores with many septa.

Thallus crustose, corticolous, pale greyish to greenish grey, rugose rimose-areolate to areolate, continuous, thickness 0.6 mm. Soredia and isidia absent. Apothecia scattered, 0.3–0.95(–1.0) mm diam., sessile, convex, constricted at the base, smooth when young, red. Disc orange-yellow to brownish yellow, white pruina present when young but absent when mature; Thalline margin well developed; amphithecium present, 70–90 μm thick.

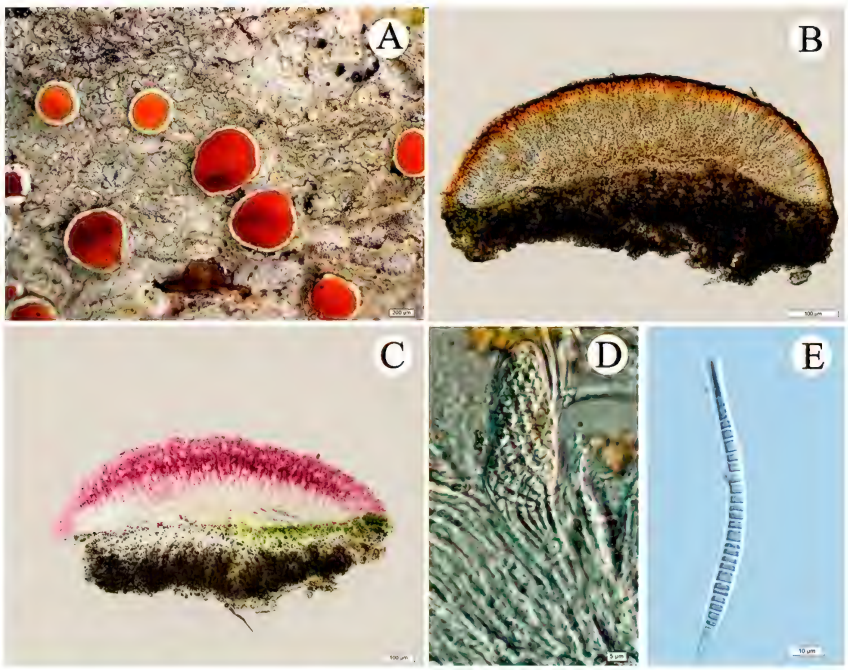

Fig. 1. ***Haematomma pluriseptatum*** (holotype, SDNU (Wang Chunxiao 20181135)). A. Thallus and apothecia; B. Apothecium section; C. K+ reaction (red) of epihymenium and outer exciple; D. Ascus; E. Ascospores. Scale bars: A = 200 μm; B, C = 100 μm; D = 5 μm; E = 10 μm.

Epihymenium orange, K+ red, 9–20 μm thick. Hymenium hyaline, 70–95 μm high. Hypothecium hyaline or slightly brown. Paraphyses branched and anastomosing. Asci clavate, containing 8 spores. Ascospores twisted in ascus, filiform, straight or slightly curved, (19–)20–26(–27)-septate, 70–95 × 5–6.5(–7) μm. Conidia absent.

Chemistry—Cortex K+ yellow, C–, KC–. Atranorin, russulone, and pseudoplacodiolic acid detected by TLC.

Additional specimens examined: **China. Yunnan, Diqing Co.**, Shangri-La, Tianbao Mt., 27°36′37″N 99°53′37″E, alt. 3790 m, on bark of living trees, 17 Aug. 2018, Wang Chunxiao 20181175, 20181209, 20181126 (SDNU); **Deqin Co.**, Yubeng Village, Xiaonong Base Camp. 28°23.92′N 98°46.16′E, alt. 3500 m, on bark of living trees, 14 Sep. 2012, Niu Dongling 12–36322 (KUN-L).

Comments—*Haematomma pluriseptatum* is characterized by the large number of septa (20–27) in each ascospore and the presence of atranorin, russulone and pseudoplacodiolic acid in the thallus.

The new ascomycete is morphologically similar to *H. rufidulum* (Fée) A. Massal., which differs by the occurrence of slightly irregular, white, convex to hemispherical soredia and elongate-fusiform, 8–25-celled, 50–72(–85) × (3.5–)4–6(–7) µm ascospores (Brodo & al. 2008). Secondary metabolites also differ: *H. pluriseptatum* contains pseudoplacodiolic acid, while *H. rufidulum* contains placodiolic acid.

Haematomma pluriseptatum may also be confused with *H. dolichosporum* (B. de Lesd.) Kalb & Staiger, which also produces twisted spores in the asci, but *H. dolichosporum* is readily distinguished by its shorter (42–62 µm) spores with fewer (7–9(–11)) septa and the production of placodiolic acid (Staiger & Kalb 1995; Brodo & al. 2008).

Key to the species of *Haematomma* in China

1. Epihymenium with russulone, K+ red 2
1. Epihymenium with haematommone, K+ purple (entirely dissipating) 8
2. Thallus containing usnic acid ..... ***H. fauriei***
2. Thallus lacking usnic acid 3
3. On rock ..... ***H. fenzlianum***
3. On bark 4
4. Thallus containing placodiolic acid ..... ***H. rufidulum***
4. Thallus lacking placodiolic acid 5
5. Thallus lacking sphaerophorin 6
5. Thallus containing sphaerophorin, spores 6–14-celled 7
6. Thallus containing pseudoplacodiolic acid, spores 20–27–celled ..... ***H. pluriseptatum***
6. Thallus lacking pseudoplacodiolic acid, spores 8–16–celled ..... ***H. puniceum* subsp. *pacificum***
7. Spores 6–7-celled ..... ***H. persoonii***
7. Spores 10–14-celled ..... ***H. collatum***
8. Spores not submuriform 9
8. Spores submuriform ..... ***H. wattii***
9. Apothecia sorediate ..... ***H. caperaticum***
9. Apothecia not sorediate 10
10. Thallus containing isoplacodiolic, isopseudoplacodiolic acids ..... ***H. flexuosum***
10. Thallus lacking isoplacodiolic, isopseudoplacodiolic acids 11
11. Spores 7–12-celled ..... ***H. accolens***
11. Spores 17–24-celled ..... ***H. africanum***

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New records of *Didymium inconspicuum*, *D. karstensii*, and *D. rugulosporum* from China

Chaofeng Yuan, Shu Li, Wan Wang, Shuwei Wei, Qi Wang*, Yu Li

Engineering Research Center of Chinese Ministry of Education for Edible and Medicinal Fungi, Jilin Agricultural University, Changchun, Jilin 130118 China

* Correspondence to: *qiwang@jiau.edu.cn*

Abstract—*Didymium inconspicuum, D. karstensii,* and *D. rugulosporum* are reported as new records for China. Morphological characteristics were observed and described by light microscopy and scanning electron microscopy and are discussed and compared with similar species.

Key words—*Didymiaceae, Myxogastrea*, taxonomy

Introduction

Didymium was introduced by Schrader (Schrader 1797) and characterized by sporophores with a peridium covered with stellate lime crystals. In contrast, the capillitium is almost always limeless. The lime crystal nature on the peridium separates *Didymium* from *Diderma*, in which the lime occurs as amorphous granules (Martin & Alexopoulos 1969). Currently *Didymium* includes approximately 94 species around the world (Kirk & al. 2008, Lado 2018), of which 35 have been recorded in China (Li & al. 1996, Liu & Chen 1998, Chen 1999, Li 2008, **Liu & Chang 2011,** Gao & al. 2018). The objectives of this work were to examine some putative *Didymium* samples, characterize them by light and scanning electron microscopy, and compare them with similar species.

Materials & methods

Specimen collection and moist chamber culture

Didymium rugulosporum was collected from Huzhong Nature Reserve, Heilongjiang Province in 2016. *Didymium karstensii* was collected from Changbai Mountain, Jilin Province in 2018. *Didymium inconspicuum* was collected from the desert transition zone of Suwu Township, Minqin County, Gansu Province in 2016. The specimens are deposited in the Herbarium of the Mycological Institute of Jilin Agricultural University, Changchun, China (HMJAU).

Morphological identification

The morphological characteristics of the sporocarps were observed by light microscope and scanning electron microscope. Each sporocarp was placed on a slide and one drop of 4% KOH added. The slide cover was placed on top and gently tapped, and filter paper used to remove excess solution. The capillitium, calcareous crystals, and spores were observed under a Leica DM 2000 light microscope (LM). Up to 20 spores were randomly selected and their diameters measured. The ultrastructure was observed under the Hitachi SU8010 scanning electron microscope (SEM) operating at 5kV (Martin & Alexopoulos 1969, Zhu & al. 2012, Li & al. 2017).

Taxonomy

Didymium inconspicuum Nann.-Bremek. & D.W. Mitch.,
Proc. Kon. Ned. Akad. Wetensch., C 92: 508. 1989 Fig. 1

Sporocarps sessile, scattered, occasionally mingled with short plasmodiocarps, small and inconspicuous. 0.5–1 mm long, about 0.5 mm high, ovoid, often depressed in the center, grayish white. Columella absent. Peridium membranous, thin, coated with grayish white lime crystals. Capillitium profuse, threads slender and curved, pale brown, 1–1.5 μm diam., often branching and anastomosing to an incomplete network, sometimes with flattened and darker colored sections on the branches. Spores dark brown in mass, brown by LM, ovoid to globose, 8–11 μm diam., evenly slightly warted.

Specimen examined: **CHINA, Gansu Province, Minqin County**, Suwu Township, 38°16′42″N 103°06′17″E, 1360 m, on leaf by moist chamber culture, 16 September 2016, Chaofeng Yuan & Shuwei Wei (HMJAU 10650).

Comments: *Didymium inconspicuum* is similar to *Didymium obducens* P. Karst. [= *D. fulvum* Sturgis] and *Didymium ochroideum* G. Lister. The spore of *D. obducens* is tuberculate on one side, while the other side is smooth and the color is pale, but the spore of *D. inconspicuum* has relatively uniform small warts. The spore of *D. ochroideum* is 6–8 μm diam. whereas the spore of *D. inconspicuum* is 8–11 μm diam.

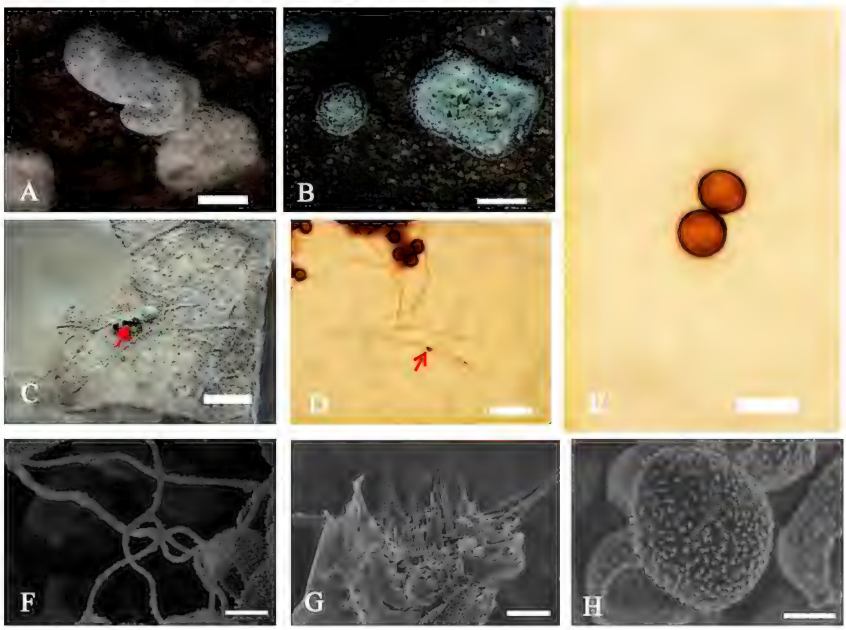

Fig 1. *Didymium inconspicuum*. A– C. Sporocarps; D. Capillitium (LM); E. Spores (LM); F. Capillitium (SEM); G. Lime crystal (SEM); H. Spores (SEM). Scale bars: A– C = 500 µm; D, F = 10 µm; E, G, H = 5 µm.

Nannenga-Bremekamp (1989) described *D. inconspicuum* as having white or pale yellow-brown tiny lime crystals, with a coarse capillitium and spores that are 12–14(–15) µm diam.; Schnittler & Novozhilov (2000) described this species as having 3–6 µm long lime crystals smaller than spores, a pale to pale brown, 1–2(–2.5) µm diam. capillitium, and (9.5–)10.5–11.5(–12.5) µm diam. spores. Our specimen has white lime crystals about 5–8 µm diam., a light brown 1–1.5 µm diam. capillitium, and spores 8–11 µm diam.; other features are consistent with the published descriptions.

Didymium karstensii Nann.-Bremek., Acta Bot. Neerl. 13: 247. 1964 Fig. 2

Sporocarps gregarious, sessile or with a short stalk, white, subglobose, 1 mm wide, up to 0.5 mm high, stalk (when present) calcareous, yellowish white, about 0.2 mm long. Peridium double, outer layer white, with stellate lime crystals about 5 µm diam. forming the wrinkled shell; the inner layer membranous and colorless. Columella white, calcareous, slightly thickened at

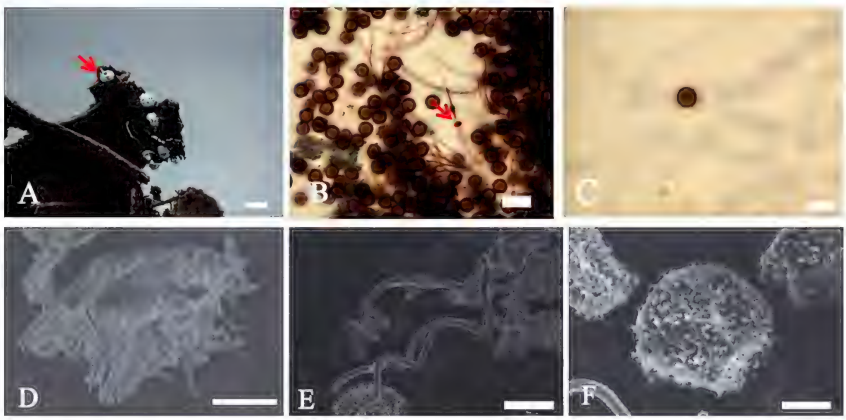

Fig 2. *Didymium karstensii*. A. Sporocarps; B. Capillitium and swelling (LM); C. Spores (LM); D. Lime crystals (SEM); E. Capillitium (SEM); F. Spores (SEM). Scale bars: A = 1 mm; B–E = 10 μm; F = 5 μm.

the base. Capillitium pale brown, threads slender, branching and anastomosing to a network, with dark swellings, 2–3 μm diam., attached to the peridium and to the base of the sporocarp. Spores dark brown in mass, brown by LM, densely warted and ridged, 7.5–10 μm diam.

Specimen examined: **CHINA, Jilin Province, Changbai Mountain,** 42°22′18″N 128°00′14″E, 828 m, on the leaf, 5 September 2018, Chaofeng Yuan & Shuwei Wei (HMJAU 10651).

Comments: *Didymium karstensii* is similar to *Didymium squamulosum* (Alb. & Schwein.) Fr., but *D. karstensii* is inconspicuously umbilicate at the base, whereas *D. squamulosum* is deeply umbilicate at the base. Nannenga-Bremekamp (1964) described stalks of *D. karstensii* as generally not exceeding half the diameter of the sporocarps, and spinulose spores, 10–12 μm diam. Demirel & Kaşik (2012) described stalks of *D. karstensii* generally not exceeding 0.2 mm long, and warted spores, 10–12 μm diam. Our specimen had stalks about 0.2 mm long and warted spores, 7.5–10 μm across; other features are consistent with the published descriptions.

Didymium rugulosporum Kowalski, Mycologia 61: 636. 1969 Fig. 3

Sporocarps sessile, scattered to clustered, globose to subglobose, 1–2.5 mm diam., white. Peridium double, the outer layer thick and fragile, white smooth calcareous shell, stellate lime crystals; the inner layer membranous, thin, colorless and transparent. Columella absent. Capillitium dense, rigid, brown,

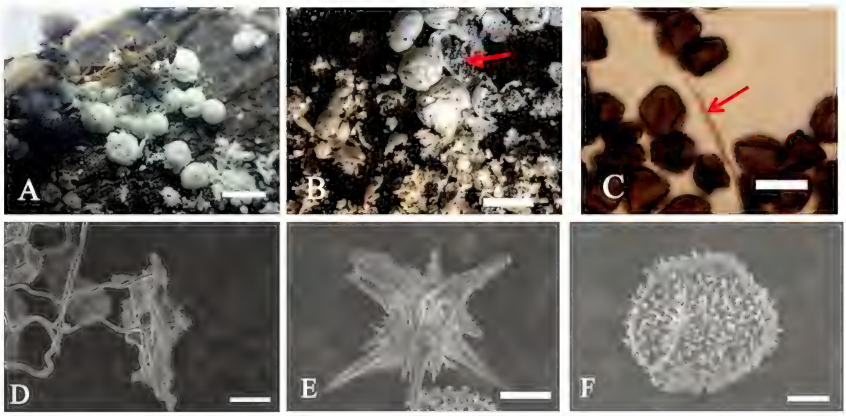

Fig 3. *Didymium rugulosporum*. A, B. Sporocarps; C. Capillitium and spores (LM); D. Capillitium and peridium (SEM); E. Lime crystal (SEM); F. Spores (SEM). Scale bars: A, B = 1 mm; C = 20 μm; D = 10 μm; E, F = 5 μm.

1–1.5 μm diam., weakly attached to the base and apex of the sporocarps, brown, branched with many colorless swellings. Spores dark brown in mass, purple brown by LM, globose, 17–19 μm diam., with large dense warts about 1.5 μm high and with some ridges forming a reticulum.

Specimen examined: **CHINA, Heilongjiang Province, Huzhong Nature Reserve**, 52°06′02″N 123°20′38″E, 168 m, on the bark, 24 September 2016, Wan Wang (HMJAU 10652).

Comments: *Didymium rugulosporum* is similar to *Didymium trachysporum* G. Lister and *Didymium quitense* (Pat.) Torrend, which differ by their smaller spores (*D. trachysporum* 9–10 μm diam.; *D. quitense* is 12–15 μm diameter). Kowalski (1969) described spores of *D. rugulosporum* as (16–)18–20(–22) μm diam. Our specimen had spores 17–19 μm diam.; other characteristics are consistent with the original description.

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Rhomboidia wuliangshanensis gen. & sp. nov. from southwestern China

Tai-Min Xu[1,2], Xiang-Fu Liu[3], Yu-Hui Chen[2], Chang-Lin Zhao[1,3*]

[1] *Yunnan Provincial Innovation Team on Kapok Fiber Industrial Plantation;*
[2] *College of Life Sciences;* [3] *College of Biodiversity Conservation:*
Southwest Forestry University, Kunming 650224, P.R. China

[*] Correspondence to: *fungichanglinz@163.com*

Abstract—A new, white-rot, poroid, wood-inhabiting fungal genus, *Rhomboidia*, typified by *R. wuliangshanensis*, is proposed based on morphological and molecular evidence. Collected from subtropical Yunnan Province in southwest China, *Rhomboidia* is characterized by annual, stipitate basidiomes with rhomboid pileus, a monomitic hyphal system with thick-walled generative hyphae bearing clamp connections, and broadly ellipsoid basidiospores with thin, hyaline, smooth walls. Phylogenetic analyses of ITS and LSU nuclear RNA gene regions showed that *Rhomboidia* is in *Steccherinaceae* and formed as distinct, monophyletic lineage within a subclade that includes *Nigroporus*, *Trullella*, and *Flabellophora*.

Key words—*Polyporales,* residual polyporoid clade, taxonomy, wood-rotting fungi

Introduction

Polyporales Gäum. is one of the most intensively studied groups of fungi with many species of interest to fungal ecologists and applied scientists (Justo & al. 2017). Species of wood-inhabiting fungi in *Polyporales* are important as saprobes and pathogens in forest ecosystems and in their application in biomedical engineering and biodegradation systems (Dai & al. 2009, Levin & al. 2016). With roughly 1800 described species, *Polyporales* comprise about 1.5% of all known species of Fungi (Kirk & al. 2008). Currently, there are 46 genomes of polyporalean taxa available from the Joint Genome Institute MycoCosm portal (Grigoriev & al. 2013).

Table 1. Species and sequences used in the phylogenetic analyses

Species	Sample	GenBank accession no.		References
		ITS	LSU	
Abortiporus biennis	TFRI 274	EU232187	EU232235	Larsson 2007
Antrodiella americana	Gothenburg 3161	JN710509	JN710509	Miettinen & al. 2012
A. semisupina	FCUG 960	EU232182	EU232266	Binder & al. 2005
Antrodiella sp.	X 418	JN710523	JN710523	Miettinen & al. 2012
Climacocystis borealis	KH 13318	JQ031126	JQ031126	Binder & al. 2013
Diplomitoporus flavescens	X 84	FN907908	—	Miettinen & al. 2012
Elaphroporia ailaoshanensis	CLZhao 595	MG231568	MG231568	Wu & al. 2018
	CLZhao 596	MG231572	MG231572	Wu & al. 2018
Flabellophora sp.	X340	JN710534	JN710534	Miettinen & al. 2012
Flaviporus brownii	X 1216	JN710537	JN710537	Miettinen & al. 2012
F. liebmannii	X 251	JN710541	JN710541	Miettinen & al. 2012
	X 249	JN710539	JN710539	Miettinen & al. 2012
	X 666	JN710540	JN710540	Miettinen & al. 2012
Frantisekia mentschulensis	BRNM 710170	FJ496728	—	Tomšovský & al. 2010
	1377	JN710544	JN710544	Miettinen & al. 2012
Hypochnicium bombycinum	MA 15305	FN552537	—	Binder & al. 2013
H. lyndoniae	NL 041031	JX124704	JX124704	Binder & al. 2005
Irpex lacteus	CBS 431.48	MH856423	MH867969	Vu & al. 2019
	DO 421/951208	JX109852	JX109852	Binder & al. 2013
Ischnoderma benzoinum	KHL 12099	JX109841	JX109841	Binder & al. 2013
I. resinosum	FD-328	KP135303	KP135225	Floudas & Hibbett 2015
Junghuhnia crustacea	X 1127	JN710554	JN710554	Miettinen & al. 2012
	X 262	JN710553	JN710553	Miettinen & al. 2012
J. micropora	Spirin 2652	JN710559	JN710559	Miettinen & al. 2012
Loweomyces fractipes	X 1149	JN710570	JN710570	Miettinen et al. 2012
	X 1253	JN710569	JN710569	Miettinen & al. 2012
	X 1250	JN710568	JN710568	Miettinen & al. 2012
Mycorrhaphium adustum	8024	JN710573	JN710573	Miettinen & al. 2012
	Dai 10173	KC485537	KC485554	—

Nigroporus vinosus	X 839	N710576	N710576	Miettinen & al. (012
	8182	JN710728	JN710728	Miettinen & al. 2012
	BHS2008-100	JX109857	JX109857	Binder & al. 2013
Panus conchatus	X 1234	JN710579	JN710579	Miettinen & al. 2012
P. strigellus	INPA 243940	JQ955725	JQ955732	Binder & al. 2013
Physisporinus sanguinolentus	BRNM 699576	FJ496671	FJ496725	Tomšovský & al. 2010
P. vitreus	3163	JN710580	JN710580	Miettinen & al. 2012
	KHL11959	JQ031129	JQ031129	Sjökvist & al. 2012
	CBS 486.72	MH860538	MH872244	Vu & al. 2019
Podoscypha venustula	CBS 65684	JN649367	JN649367	Binder & al. 2013
Pseudolagarobasidium acaciicola	CBS 115543	DQ517883	—	Miettinen & Rajchenberg 2012
	CBS 115544	DQ517882	—	Miettinen & Rajchenberg 2012
P. belizense	CFMR DLC 04-31	JQ070173	—	Miettinen & Rajchenberg 2012
Rhomboidia wuliangshanensis	**CLZhao 4406 [T]**	MK860715	MK860710	Present study
	CLZhao 4411	MK860716	MK860711	Present study
Skeletocutis novae-zelandiae	Ryvarden 38641	JN710582	JN710582	Miettinen & al. 2012
Spongipellis spumeus	PRM 891931	HQ728287	HQ729021	Tomšovský & al. 2010
	BRNM 712630	HQ728288	HQ728288	Tomšovský & al. 2010
	BRNM 734877	HQ728283	HQ728283	Tomšovský & al. 2010
Steccherinum fimbriatum	KHL 11905	EU118668	EU118668	Tomšovský & al. 2010
S. ochraceum	Ryberg s.n.	EU118669	EU118670	Larsson 2007
	KHL 11902	JQ031130	JQ031130	Sjökvist & al. 2012
Trullella dentipora	X 200	JN710512	JN710512	Miettinen & al. 2012
T. duracina	X 290	JN710513	JN710513	Miettinen & al. 2012
T. polyporoides	X 510	JN710602	JN710602	Miettinen & al. 2012
Xanthoporus syringae	X 339	JN710606	JN710606	Miettinen & al. 2012
	Cui 2177	DQ789395	—	Miettinen & al. 2012
	Gothenburg 1488	JN710607	JN710607	Miettinen & al. 2012

Systematics of the *Polyporales* has benefitted from numerous molecular phylogenetic studies (e.g., Binder & al. 2005, 2013; Larsson 2007; Miettinen & al. 2012; Dai & al. 2015; Choi & Kim 2017). *Steccherinaceae* Parmasto, one of 18 families recognized in *Polyporales* (Justo & al. 2017), has been included in several molecular studies (e.g., Binder & al. 2005, 2013; Miettinen & al. 2012; Miettinen & Ryvarden 2016; Justo & al. 2017; Westphalen & al. 2018). Miettinen & al. (2012) published a multigene, molecular phylogenetic study of *Steccherinum* and allied taxa that clearly delineated *Steccherinaceae*. They uncovered surprising morphological diversity and plasticity in this family, requiring revision of generic concepts and 15 new genera to accommodate existing and new species. Subsequently, Miettinen & Ryvarden (2016) introduced five new genera, revised one genus, and described two new species that had been identified earlier by Miettinen & al. (2012). Justo & al. (2017), who revised family-level classification in *Polyporales,* confirmed *Steccherinaceae* as a distinct lineage in *Polyporales* that grouped with *Cerrenaceae* Miettinen & al. and *Panaceae* Miettinen & al. In a morphological and molecular study of Neotropical taxa of *Junghuhnia* and *Steccherinum*, Westphalen & al. (2018) uncovered a new genus and several new species and reclassified four taxa.

Cosmopolitan in distribution, *Steccherinaceae* has a rich diversity because it is found in boreal, temperate, subtropical, and tropical ecosystems (Núñez & Ryvarden 2001, Dai 2012, Ryvarden & Melo 2014, Dai & al. 2015, Zhou & al. 2016). Many new species in *Polyporales* have been described from southern, subtropical China (e.g., Li & Cui 2010, Zhao & Wu 2017, Zhao & Ma 2019). Recently, we collected an undescribed taxon from Yunnan Province that could not be assigned to any described genus. We present morphological and molecular phylogenetic evidence that support the recognition of a new monotypic genus in *Steccherinaceae—Rhomboidia*, typified by *R. wuliangshanensis*.

Materials & methods

The specimens studied are deposited at the herbarium of Southwest Forestry University, Kunming, China (SWFC). Macromorphological descriptions are based on field notes. Special colour terms follow Petersen (1996). Micromorphological data were obtained from the dried specimens and observed under a light microscope following Dai (2010). The following abbreviations are used: KOH = 5% potassium hydroxide; CB = cotton blue; CB– = acyanophilous; IKI = Melzer's reagent; IKI– = non-amyloid and non-dextrinoid; L = mean spore length (arithmetic average of all spores); W = mean spore width (arithmetic average of all spores); Q = variation in

the L/W ratios between the specimens studied; (n = a/b) = number of spores (a) from number of specimens (b).

HiPure Fungal DNA Mini Kit II was used to obtain genomic DNA from dried specimens, according to the manufacturer's instructions with some modifications. A small piece (about 30 mg) of dried fungal material was ground to powder with liquid nitrogen. The powder was transferred to a 1.5 ml centrifuge tube, suspended in 0.4 ml of lysis buffer, and incubated in a 65 °C water bath for 60 min. After that, 0.4 ml phenol-chloroform (24:1) was added to each tube and the suspension was shaken vigorously. After centrifugation at 13,000 rpm for 5 min, 0.3 ml supernatant was transferred to a new tube and mixed with 0.45 ml binding buffer. The mixture was then transferred to an adsorbing column (AC) for centrifugation at 13,000 rpm for 0.5 min. Then, 0.5 ml inhibitor removal fluid was added in AC for a centrifugation at 12,000 rpm for 0.5 min. After washing twice with 0.5 ml washing buffer, the AC was transferred to a clean centrifuge tube, and 100 ml elution buffer was added to the middle of adsorbed film to elute the genomic DNA. The internal transcribed spacer region (ITS) was amplified with primer pairs ITS5 and ITS4 (White & al. 1990). The nuclear large subunit region (LSU) was amplified with primer pairs LR0R and LR7 (https://sites.duke.edu/vilgalyslab/rdna_primers_for_fungi/). The PCR procedure for ITS was: initial denaturation at 95 °C for 3 min, followed by 35 cycles of 94 °C for 40 s, 58 °C for 45 s, and 72 °C for 1 min; and a final extension of 72 °C for 10 min. The PCR procedure for LSU was: initial denaturation at 94 °C for 1 min, followed by 35 cycles of 94 °C for 30 s, 48 °C 1 min, and 72 °C for 1.5 min; and a final extension of 72 °C for 10 min. The PCR products were purified and directly sequenced at Kunming Tsingke Biological Technology Limited Company. All newly generated sequences were deposited at GenBank (Table 1).

Sequencher 4.6 was used to edit the DNA sequence. Sequences were aligned in MAFFT 6 (Katoh & Toh 2008, http://mafft.cbrc.jp/alignment/server/) using the "G-INS-I" strategy and manually adjusted in BioEdit (Hall 1999). The sequence alignment was deposited in TreeBase (submission ID 24216). *Xanthoporus syringae* (Parmasto) Audet obtained from GenBank was used as an outgroup to root trees following Miettinen & al. (2012) in the ITS+LSU analyses (Fig. 1).

The ITS+LSU sequences were analyzed phylogenetically using maximum parsimony, maximum likelihood, and Bayesian inference methods. Maximum parsimony (MP) analyses followed Zhao & Wu (2017), and tree construction was performed in PAUP* version 4.0b10 (Swofford 2002). All characters were equally weighted and gaps were treated as missing data. Trees were inferred using the heuristic search option with TBR branch swapping and 1000 random sequence additions. Max-trees was set to 5000, branches of zero length were collapsed and all parsimonious trees were saved. Clade robustness was assessed using bootstrap (BP) analysis with 1000 replicates (Felsenstein 1985). Tree statistics tree length (TL), consistency index (CI), retention index (RI), rescaled consistency index (RC), and homoplasy index (HI) were calculated for each Maximum Parsimonious Tree generated. Sequences were analyzed using Maximum Likelihood (ML) with

RAxML-HPC2 through the Cipres Science Gateway (www.phylo.org; Miller & al. 2009). Branch support (BS) for ML analysis was determined by 1000 bootstrap replicates.

MrModeltest 2.3 (Posada & Crandall 1998; Nylander 2004) was used to determine the best-fit evolution model for data set for Bayesian inference (BI). Bayesian inference was calculated with MrBayes_3.1.2 using a general time reversible (GTR+G) model of DNA substitution and a gamma distribution rate variation across sites (Ronquist & Huelsenbeck 2003). Four Markov chains were run for 2 runs from random starting trees for 4 million generations (ITS+LSU) in Fig. 1 and trees were sampled every 100 generations. The first 25% of the generations were discarded as burn-in. A majority rule consensus tree of all remaining trees was calculated. Branches that received bootstrap support for maximum likelihood (BS) ≥75%, maximum parsimony (BP) ≥75%, and Bayesian posterior probabilities (BPP) ≥0.95 were considered significantly supported.

Molecular phylogenetic results

The ITS+LSU (Fig. 1) dataset comprised sequences from 55 fungal specimens representing 34 taxa, including the outgroup taxon. The dataset had an aligned length of 2296 of which 1395 were constant, 201 parsimony-uninformative, and 700 parsimony-informative. MP analysis yielded two equally parsimonious trees (TL = 3897, CI = 0.376, HI = 0.624, RI = 0.627, RC = 0.236). The best-fit model for ITS+LSU alignment estimated and applied in the BI was GTR+I+G, lset nst = 6, rates = invgamma; prset statefreqpr = dirichlet (1,1,1,1). BI resulted in a similar topology with an average standard deviation of split frequencies equal to 0.006862.

Rhomboidia wuliangshanensis forms a monophyletic lineage with strong support (BS = 100%, BP = 100%, BPP = 1) and is sister to the *Nigroporus–Trullella* clade (Fig. 1).

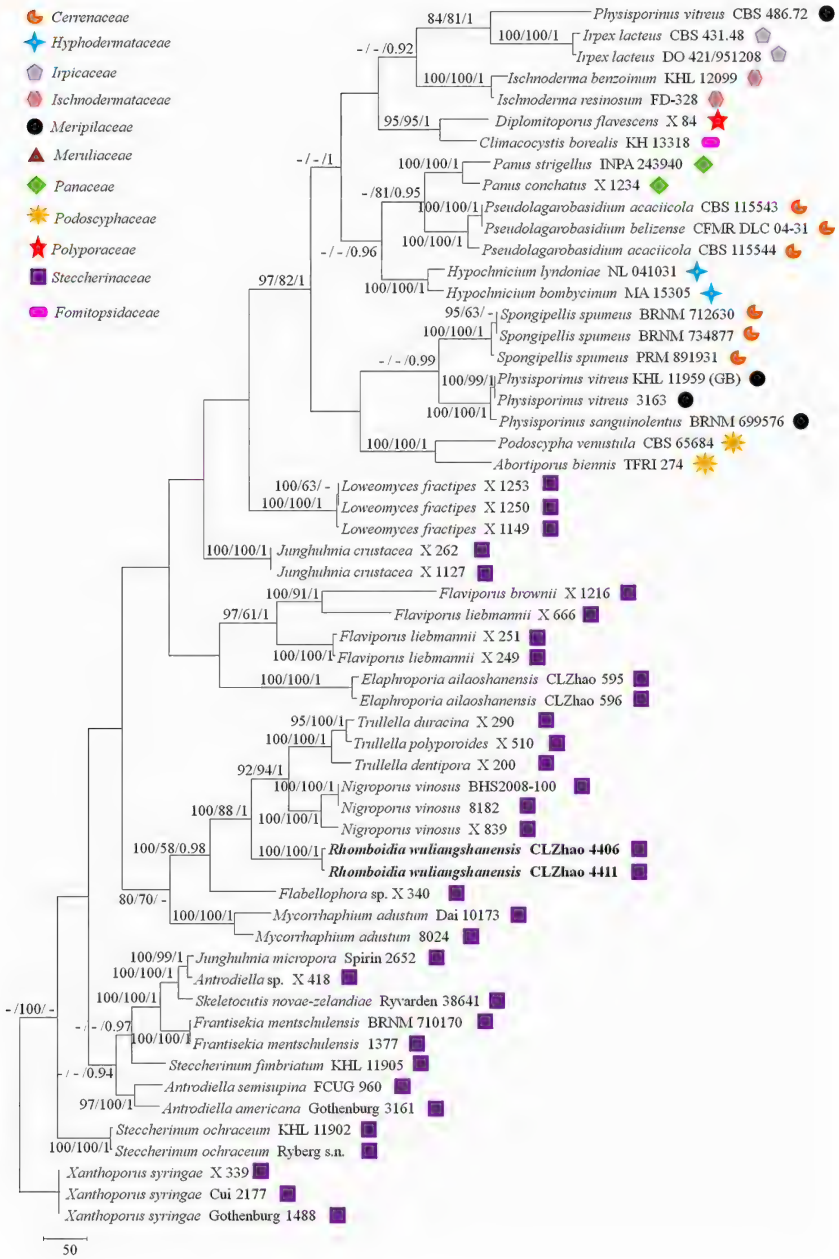
Taxonomy

Rhomboidia C.L. Zhao, **gen. nov.**

MB 833318

Differs from *Nigroporus* and *Trullella* by its stipitate to substipitate basidiomata, its orange-brown to reddish brown surface, and its monomitic hyphal system in both context and trama.

Fig. 1. Maximum parsimony strict consensus tree illustrating the phylogeny of *Rhomboidia wuliangshanensis* and related species in the residual polyporoid clade based on ITS+nLSU sequences. Branches are labeled with maximum likelihood bootstrap >70%, parsimony bootstrap proportions >50% and Bayesian posterior probabilities >0.95.


Cerrenaceae
Hyphodermataceae
Irpicaceae
Ischnodermataceae
Meripilaceae
Meruliaceae
Panaceae
Podoscyphaceae
Polyporaceae
Steccherinaceae
Fomitopsidaceae
Physisporinus vitreus CBS 486.72
Irpex lacteus CBS 431.48
Irpex lacteus DO 421/951208
Ischnoderma benzoinum KHL 12099
Ischnoderma resinosum FD-328
Diplomitoporus flavescens X 84
Climacocystis borealis KH 13318
Panus strigellus INPA 243940
Panus conchatus X 1234
Pseudolagarobasidium acaciicola CBS 115543
Pseudolagarobasidium belizense CFMR DLC 04-31
Pseudolagarobasidium acaciicola CBS 115544
Hypochnicium lyndoniae NL 041031
Hypochnicium bombycinum MA 15305
Spongipellis spumeus BRNM 712630
Spongipellis spumeus BRNM 734877
Spongipellis spumeus PRM 891931
Physisporinus vitreus KHL 11959 (GB)
Physisporinus vitreus 3163
Physisporinus sanguinolentus BRNM 699576
Podoscypha venustula CBS 65684
Abortiporus biennis TFRI 274
Loweomyces fractipes X 1253
Loweomyces fractipes X 1250
Loweomyces fractipes X 1149
Junghuhnia crustacea X 262
Junghuhnia crustacea X 1127
Flaviporus brownii X 1216
Flaviporus liebmannii X 666
Flaviporus liebmannii X 251
Flaviporus liebmannii X 249
Elaphroporia ailaoshanensis CLZhao 595
Elaphroporia ailaoshanensis CLZhao 596
Trullella duracina X 290
Trullella polyporoides X 510
Trullella dentipora X 200
Nigroporus vinosus BHS2008-100
Nigroporus vinosus 8182
Nigroporus vinosus X 839
Rhomboidia wuliangshanensis CLZhao 4406
Rhomboidia wuliangshanensis CLZhao 4411
Flabellophora sp. X 340
Mycorrhaphium adustum Dai 10173
Mycorrhaphium adustum 8024
Junghuhnia micropora Spirin 2652
Antrodiella sp. X 418
Skeletocutis novae-zelandiae Ryvarden 38641
Frantisekia mentschulensis BRNM 710170
Frantisekia mentschulensis 1377
Steccherinum fimbriatum KHL 11905
Antrodiella semisupina FCUG 960
Antrodiella americana Gothenburg 3161
Steccherinum ochraceum KHL 11902
Steccherinum ochraceum Ryberg s.n.
Xanthoporus syringae X 339
Xanthoporus syringae Cui 2177
Xanthoporus syringae Gothenburg 1488
50

Type species: *Rhomboidia wuliangshanensis* C.L. Zhao

Etymology: *Rhomboidia* (Lat.): referring to the rhomboid pileus of the basidiocarp with the poroid hymenophore.

Basidiomata annual, stipitate. Pileus rhomboid, arising from a multiple branched stipe. Pores angular, small, dissepiments thin, entire. Hyphal system monomitic; generative hyphae thick-walled bearing clamp connections, IKI–, CB–; tissues unchanged in KOH. Cystidia absent, fusoid cystidioles numerous; hyphal ends numerous. Basidia barrel-shaped to clavate. Basidiospores broadly ellipsoid, hyaline, thin-walled, smooth, IKI–, CB–.

Type of rot: white rot.

Rhomboidia wuliangshanensis C.L. Zhao, **sp. nov.** Figs 2, 3

MB 833320

Differs from *Nigroporus vinosus* by its stipitate to substipitate basidiomata and monomitic hyphal structure.

Type: China. Yunnan Province: Puer, Jingdong County, Wuliangshan National Nature Reserve, on angiosperm trunk, 6 Oct 2017, CLZhao 4406 (**Holotype**, SWFC 0004406; GenBank MK860715, MK860710).

Etymology: The specific epithet *wuliangshanensis* (Lat.) refers to the type locality, Wuliangshan.

Basidiomata annual, stipitate to substipitate. Pileus rhomboid, arising from a multiple branched stipe, edges curling slightly inward, 3.5 cm from the base to margin, 4 cm wide, up to 3 mm thick; pileus surface radially striate, slightly brown to orange brown when fresh, drying brown to reddish; the margin acute, entire. Pore surface white when fresh, cream to buff upon drying. Pores angular, 7–9 per mm, dissepiments thin, entire. Context corky, white, thin, up to 0.5 mm thick. Tubes concolorous with pore surface, corky, up to 2.5 mm long.

-Type of rot: white rot.

Additional specimen examined: **CHINA. Yunnan province. Puer:** Jingdong County, Wuliangshan National Nature Reserve, on angiosperm trunk, 6 Oct 2017, CLZhao 4411 (SWFC 004411; GenBank MK860716, MK860711).

Discussion

Rhomboidia is supported as a new genus by phylogenetic analyses and morphological characters. It is embedded in *Steccherinaceae* with strong support. Phylogenetically, *Rhomboidia* is closely related to *Flabellophora* G. Cunn., *Nigroporus* Murrill, and *Trullella* Zmitr. based on ITS+LSU nuclear RNA gene analyses (Fig. 1), which is similar to the previous multigene sequence-based study (Miettinen & al. 2012). The genera closely related to *Rhomboidia*

Fig. 2. *Rhomboidia wuliangshanensis* (holotype, SWFC 0004406). Scale bars = 5 mm.

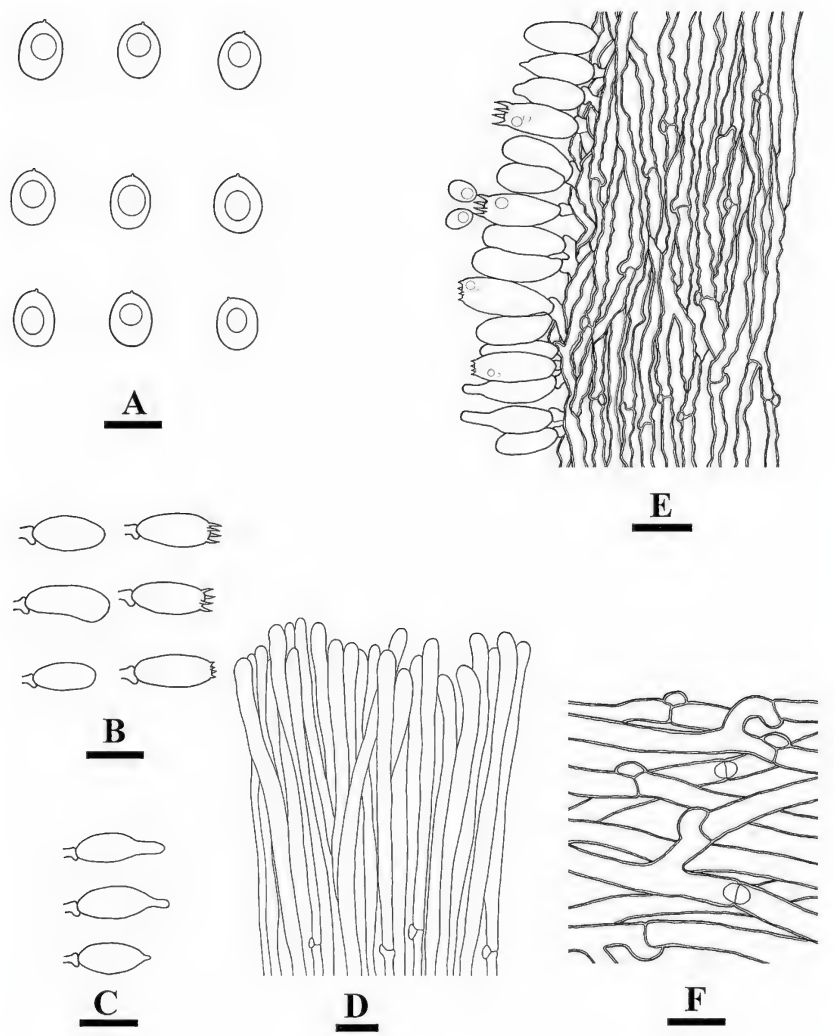


FIG. 3. *Rhomboidia wuliangshanensis* (drawn from the holotype, SWFC 0004406). A. Basidiospores; B. Basidia and basidioles; C. Cystidioles; D. Hyphal ends; E. Hyphae from trama; F. Hyphae from subiculum. Scale bars: a = 5 μm; b–f = 10 μm.

are easily separated morphologically: In *Flabellophora* basidiomata arise from a submerged pseudosclerotium and develop unilateral pilei with a crust and a coriaceous context (Núñez & Ryvarden 2001). *Nigroporus* differs from *Rhomboidia* by developing resupinate to pileate basidiocarps with vinaceous brown to pink or violet pore surface and a dimitic hyphal system (Gilbertson & Ryvarden 1987). In *Trullella* basidiomata are spathulate and light-coloured, with a monomitic hyphal system in the context but dimitic in the trama (Miettinen & al. 2012, Zmitrovich 2018).

Rhomboidia resembles other stipitate genera in *Polyporales* such as *Abortiporus* Murrill, *Jahnoporus* Nuss, and *Polyporus* P. Micheli ex Adans. *Abortiporus*, however, has a duplex structure and thick-walled basidiospores (Núñez & Ryvarden 2001). *Jahnoporus* is characterized by large spindle-shaped basidiospores (Gilbertson & Ryvarden 1987), and *Polyporus* has a dimitic hyphal system (Bernicchia & Gorjón 2010).

Polypores are extensively studied and well-known in North America (Gilbertson & Ryvarden 1987, Zhou & al. 2016) and Eurasia (Núñez & Ryvarden 2001, Bernicchia & Gorjón 2010, Dai 2012, Ryvarden & Melo 2014, Dai & al. 2015), but Chinese polypore diversity is still being explored, especially in subtropical and tropical areas. *Rhomboidia wuliangshanensis* was collected from Yunnan Province, where many new taxa in *Polyporales* and *Hymenochaetales* have been described (e.g., Li & Cui 2010, He & Li 2011, Yu & al. 2013, Yang & He 2014, Zhao & Wu 2017, Zhao & Ma 2019). We anticipate that additional, undescribed polypore taxa will be discovered throughout China after extensive collections are analyzed both morphologically and molecularly.

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Filsoniana lhasanensis sp. nov. from Tibet, China

Xue-Mei Wen[1, 2], Hurnisa Shahidin[1*], Abdulla Abbas[1*]

[1]*College of Life Science and Technology, Xinjiang University, Urumqi, 830046, P. R. China*

[2]*Tibet Plateau Institute of Biology, Lhasa, 850001, P. R. China*

* Correspondence to: *hurnisa_xju@sina.com*, *zxg_lichen@163.com*

Abstract—A new species, *Filsoniana lhasanensis*, is described from Tibet, China, where it grows on rocks at altitudes 4200–4432 m. The lichen is characterised by a poorly developed or absent dark orange areolate thallus, lecanorine to zeorine orange to deep-orange aggregated apothecia, and richly branched and anastomosed paraphyses. DNA was obtained for three gene loci—nuclear internal transcribed spacer (ITS), nuclear large subunit (LSU), and mitochondrial small subunit (SSU). Phylogenetic analyses support the taxon as a new species of *Filsoniana*.

Key words—Himalaya, phylogeny, taxonomy, *Teloschistoideae*

Introduction

Teloschistaceae is a widespread and well-delimited family of lichenized fungi, estimated at over 1000 species (Arup & al. 2013). Most species contain anthraquinone (which confers a yellow to orange color) and grow under sun-exposed conditions (Gaya & al. 2015). Recent molecular phylogenetic research supports subdivision of the *Teloschistaceae* into three subfamilies: *Xanthorioideae*, *Caloplacoideae*, and *Teloschistoideae* (Arup & al. 2013; Gaya & al. 2015). Kondratyuk & al. (2013, 2015), who evaluated *Teloschistoideae* based on three gene loci (ITS, LSU, SSU), proposed an additional subfamily *Brownlielloideae;* however this analysis was based on a hybrid sequence dataset comprising ITS and LSU data derived from

the lichen mycobiont and the SSU derived from a fungal contaminant (Vondrák & al. 2018). Many small monophyletic genera established in *Brownlielloideae* were based solely on DNA data without any distinguishing phenotypic characters, and these genera remain within the *Teloschistoideae* as proposed by Arup & al. (2013).

During our study on Chinese *Teloschistaceae*, we collected some interesting samples from the suburbs of Lhasa and Shannan in Tibet. The Tibetan plateau is a unique biogeographical region with varied landscapes, altitudinal belts, and alpine ecosystems and is considered a world center of species formation (Zhang & al. 2002). *Teloschistaceae* in this region have been inadequately studied, with only 15 species reported (Obermayer 2004; Wei 1991, 2017; Poelt & Petutschnig 1992; Poelt & Hinteregger 1993; Wei & Jiang 1986). More species are known from the neighboring Himalayan regions: India, where >74 species of *Teloschistaceae* have been recorded (Joshi & Upreti 2006, 2011; Joshi & al. 2008, 2009, 2014; Kondratyuk & al. 2018) and Nepal, where 47 species have been discovered (Olley & Sharma 2013). According to available literature, there are still large underexplored areas in the Tibet region, and additional undescribed lichenized fungi species are expected to be discovered in this poorly studied region.

Most of crustose *Teloschistaceae* species have few taxonomically significant morphological characters. Traditional species concepts based in morphology and chemistry are overly simplified for the crustose species in *Teloschistaceae*. Modern classification methods are essential for accurate taxonomic placement of rare and undescribed species. We combined sequence analyses of three gene loci—ITS, LSU, SSU—with morphological and chemical methods to describe a new species, *Filsoniana lhasanensis*. This is the first report of the genus *Filsoniana* in China.

Materials & methods

Morphology & chemistry

Specimens collected from Lhasa and Shannan, Tibet, China, were preserved in Tibet Plateau Institute of Biology, Lhasa, China (XZ) and Lichen Research Center in Arid Zone of Northwest China, Xinjiang University, Urumqi, China (XJU–L). The specimens were examined morphologically using a Shunyu SZM45 dissecting microscope and Nikon Eclipse E100 compound microscope. Colors follow RAL color system (https://www.ralcolorchart.com/) Sections for anatomical details and measurements were made manually and mounted in water. Chemical constituents were identified by thin-layer chromatography using solvent systems C (Orange & al. 2010). Thallus morphological structures were photographed with a Nikon

Table 1. Primers and cycling parameters used for PCR.

Locus	Primers	PCR settings
ITS	ITS1F (Gardes & Bruns 1993) ITS4 (White & al. 1990)	94°C–5 min; 6 cycles of: 94°C–45 sec, 57–52°C (decreasing 1°C per cycle) –55 sec, 72°C–1 min; 30 cycles of: 94°C–45 sec, 51°C–55sec, 72°C-1 min; and 72°C–7 min
LSU	AL1R (Döring & al. 2000) LR6 (Vilgalys & Hester 1990)	94°C–10 min; 6 cycles of: 94°C–1 min, 57–52°C (decreasing 1°C per cycle) –1 min, 72°C–1.2 min; 30 cycles of: 94°C–1 min, 51°C–1 min, 72°C–1.2 min; and 72°C–2 min
SSU	mrSSU1 (Zoller & al. 1999) mrSSU7 (Zhou & Stanosz 2001)	94°C–10 min; 6 cycles of: 94°C–45 sec, 57–52°C (decreasing 1°C per cycle) –55 sec, 72°C–1 min; 30 cycles of: 94°C–45 sec, 51°C–55sec, 72°C-1 min; and 72°C–7 min

DS-Fi2 Digital Camera using a Nikon MZ25 and Nikon Eclipse Ci stereomicroscope. All measurements were made using the Nikon Nis elements (D). Morphology and anatomy were described according to Vondrák & al. (2013).

DNA extraction, PCR amplification, DNA sequencing

Total genomic DNA was extracted using the Fungi Genomic DNA Extraction Kit, following manufacturer's instructions. Molecular data were generated for three loci: the nuclear internal transcribed spacer (ITS), nuclear large subunit (LSU), and mitochondrial small subunit (SSU). Primers and PCR cycling parameters used for amplification are summarized in Table 1.

Sequence analysis

The newly generated sequences were compared to GenBank database sequences using BLASTN search (http://www.ncbi.nlm.nih.gov/BLAST/). All sequences were aligned with sequences of selected representatives of *Teloschistoideae* obtained from GenBank (Table 2) using MAFFT version 7 (Katoh & Standley 2013) with G-INS-i method.

Phylogenies were generated using Bayesian inference and Maximum Likelihood (ML) methods. Bayesian inference used the best fitting model as inferred by jModel Test v2.1.6 (Darriba & al. 2012), implemented in MrBayes v3.2.6 (Ronquist & al. 2012) on the Cipres Scientific gateway (Miller & al. 2010), TrNef+I+G for ITS and LSU and HKY+I+G for SSU. Two parallel MCMCMC runs were executed, each using eight chains and 10,000,000 generations, with trees sampled every 1000th generation.

Maximum likelihood (RAxML) analyses were performed using RAxMLHPC v.8 on XSEDE (Stamatakis 2014) under the GTRGAMMA model on CIPRES Science Gateway (Miller & al. 2010). Rapid bootstrap analyses were performed with 1000 bootstrap replicates. The phylogenetic tree was drawn using FigTree ver. 1.4.3 (http://tree.bio.ed.ac.uk/software/figtree/).

Table 2. Sequences used in the phylogenetic analyses.
(Sequences generated for this study are in bold.)

Species	Voucher	ITS	LSU	SSU
*Brownliella aequa*ta	SK838 [4]	KF264627	KF264662	KF264688
	SK831 [4]	KF264626	KF264661	KF264687
B. kobeana	130318 [5]	KT456214	KT456229	KT456244
	120032 [5]	KT456212	KT456227	KT456242
B. montisfracti	SK231 [4]	KF264625	KF264660	KF264686
	SK230 [4]	KF264624	KF264659	—
Brownliella sp.	SK2013a [4]	KF264628	KF264663	—
Caloplaca sp.	Casan 242 [3]	KT291463	KT291558	KT291508
	Gaya 110 [3]	KT291456	KT291552	KT291499
Elixjohnia bermaguiana	Kondratyuk 20487 [1]	KC179299	KC179245	KC179584
E. gallowayi	Kärnefelt 997504 [1]	KC179301	KC179247	KC179586
E. jackelixii	U1402 [1]	KC179303	KC179248	KC179587
	SK910 [4]	KF264655	KF264683	KF264707
Filsoniana australiensis	SK851 [4]	KF264631	KF264665	KF264691
	SK850 [4]	KF264632	KF264666	KF264692
F. lhasanensis	**Z24, Wen 20110910-05**	**MK153161**	**MK439835**	**MK439831**
	Z19, Wen 20110901-29	**MK153160**	**MK439834**	**MK439830**
F. rexfilsonii	SK859 [4]	KF264638	KF264671	—
	SK861 [4]	KF264636	KF264670	—
Follmannia orthoclada	Frödén 1772 [1]	KC179291	KC179191	—
Haloplaca sp.	6-UA2013 [1]	KC179295	KC179203	KC179537
Harusavskia elenkinianoides	SK997 [6]	KY614404	KY614452	KY614485
	SK269 [6]	KY614405	KY614453	KY614486
Josefpoeltia parva	Frödén 1671 [1]	KC179296	KC179204	KC179539
J. sorediosa	Frödén 1593 [1]	KC179297	KC179205	KC179540
	SK992 [4]	KF264646	KF264674	KF264697
	SK991 [4]	KF264645	KF264673	KF264696
Kaernefia albocrenulata	SK245 [4]	KF264647	KF264675	KF264698
	SK246 [4]	KF264648	KF264676	KF264699
K. gilfillaniorum	SK999 [4]	KF264650	KF264678	KF264701
	SK253 [4]	KF264649	KF264677	KF264700
K. kaernefeltii	SK919 [4]	KF264651	KF264679	KF264702
	SK921 [4]	KF264652	KF264680	KF264703
Nevilleiella lateritia	SK 261 [6]	KY614427	KY614464	KY614502

Species	Voucher	ITS	LSU	SSU
	SK 878 [6]	KY614426	KY614463	KY614501
N. marchantii	SK D18 [6]	KY614425	KY614462	KY614500
Scutaria andina	PF209 [1]	KC179298	KC179242	KC179581
Sirenophila cliffwetmorei	SK A93 [6]	KY614438	KY614471	KY614513
S. eos	U1408 [1]	KC179300	KC179246	KC179585
S. gintarasii	SK D17 [6]	KY614437	KY614470	KY614512
S. maccarthyi	Karnefelt 977801 [1]	KC179304	KC179249	KC179588
Solitaria chrysophthalma	Cchr157 [3]	KT291446	KT291537	KT291484
Stellarangia elegantissima	PF 81 [1]	KC179310	KC179254	KC179593
	Cele 75 [3]	KT291454	KT291541	KT291488
Teloschistes exilis	Gaya 12 [2]	JQ301630	JQ301577	JQ301519
T. flavicans	AFTOL-ID 315 [2]	JQ301578	JQ301631	JQ301520
	Tflav103 [3]	KT291472	KT291565	KT291523
T. hosseusianus	Gaya 50 [2]	KC179318	JQ301579	JQ301521
T. hypoglaucus	PF68 [1]	KC179319	KC179256	KC179595
T. sieberianus	Tsie423 [3]	EU639655	—	KT291525
Teloschistopsis bonae-spei	PF82 [1]	KC179322	KC179257	KC179596
Ts. eudoxa	PF72 [1]	KC179324	KC179258	KC179597
Thelliana pseudokiamae	SK925 [4]	KF264633	KF264667	—
	SK926 [4]	KF264634	KF264668	—
	SK 925 [5]	KT456225	KT456240	—
	SK 926 [5]	KT456226	KT456241	—
Villophora isidioclada	USE563 [1]	KC179325	KC179266	KC179606
Villophora sp. 50	U1342 [1]	KC179330	KC179268	—
Villophora sp. 40	USE574 [1]	KC179328	KC179267	KC179607
Wetmoreana decipioides	Cadec188 [3]	KT291453	KT291540	KT291487
	SK689 [4]	KF264644	—	KF264695
W. texana	SK536 [4]	KF264658	—	KF264711
	USE527 [1]	KC179337	KC179273	KC179612
W. sp. 52	Frödén 1645 [1]	KC179334	KC179270	KC179609
W. sp. 54	Frödén 1521 [1]	KC179336	KC179272	KC179611
Xanthomendoza fallax	Gaya 33 [2]	JQ301687	JQ301580	JQ301633
Xa. ulophyllodes	**T11, Shahidin 145507**	**MK414784**	**MK439836**	**MK439832**
	T22, Shahidin 145449	**MK414785**	**MK439837**	**MK439833**
Xanthoria sp.	Gaya 31 [2]	JQ301692	JQ301591	JQ301532

Sources: [1] Arup & al. (2013); [2] Gaya & al. (2012); [3] Gaya & al. (2015);
[4] Kondratyuk & al. (2013); [5] Kondratyuk & al. (2015); [6] Kondratyuk & al. (2017).

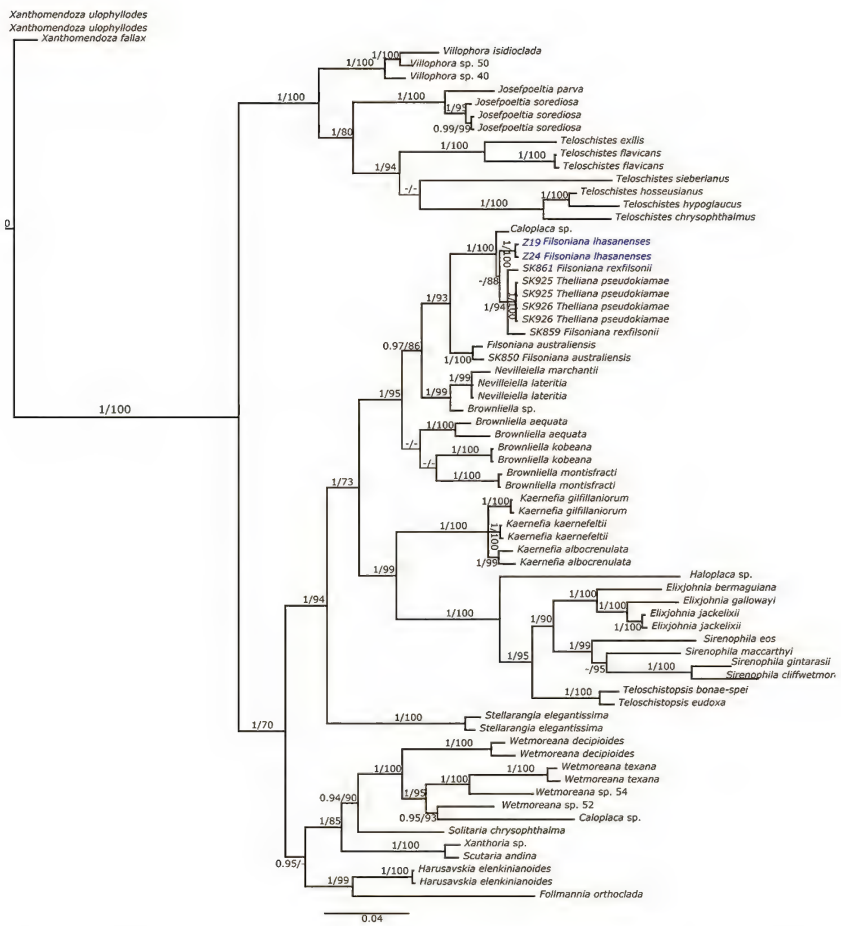

Fig. 1. The ML tree based on a concatenated 3-loci data matrix. The numbers above each node represent posterior probability (PP) and bootstrap support (BS) values. Only PP values >0.90 and BS values >70% are shown. The species described in this paper is shown in blue font.

Results & discussion

New ITS, LSU, and SSU sequences were generated in this study. A total of 70 ITS sequences, 67 LSU sequences, and 58 SSU sequences were included in the analyses (Fig. 1). Trees of similar topologies were also generated using the maximum likelihood method and Bayesian approach,

with *Xanthomendoza ulophyllodes* and *X. fallax* as outgroup. Our combined analyses grouped our new species with *Filsoniana rexfilsonii* and *Thelliana pseudokiamae* in a monophyletic clade with high support value (BS = 93, PP = 1). The new species is closely related to *Thelliana pseudokiamae* (S.Y. Kondr. & Kärnefelt) S.Y. Kondr.& al. and *F. rexfilsonii* (S.Y. Kondr. & Kärnefelt) S.Y. Kondr. & al.. Almost all other members of *Filsoniana* have well-developed thalli and occur in Australia. The sequences listed by Kondratyuk & al. (2013) under the name "*Squamulea kiamae*" were misdetermined; they were derived from specimen Kärnefelt 994101 [LD 1101337], which was resequenced by Kondratyuk & al. (2015) and designated as the holotype of a new genus and species, *Thelliana pseudokiamae* S.Y. Kondr. & al. Therefore all four of the "*Squamulea kiamae*" sequences represent *Th. pseudokiamae,* and authentic sequences of *S. kiamae* are not included in our analyses. *Filsoniana kiamae* and *Th. pseudokiamae* differ in the sorelia and lobe size (Kondratyuk & al. 2007, 2015). Our results conflict with Kondratyuk & al. (2015), whose ITS–LSU–SSU combined analyses placed *Filsoniana* in *Brownlielloideae;* our analyses place most members of *Brownlielloideae* in the *Teloschistoideae.*

Taxonomy

Filsoniana lhasanensis X.M. Wen, Shahidin & A. Abbas **sp. nov.** FIG. 2

FN 570592

Differs from *Filsoniana kiamae* and *F. rexfilsonii* by its reduced thallus, its aggregated adnate apothecia, and its Asian distribution.

TYPE: China. Tibet, Lhasa City, Maizhuokunggar county, Riduo Village, 29°42′35″N 92°05′10″E, alt. 4200 m, 1 September 2011, X. M. Wen 20110901-29 (**Holotype**, XZ; **isotype**, XJU–L; GenBank MK153160, MK439834, MK43983).

ETYMOLOGY: The epithet *lhasanensis* refers to the region in which the type specimen was collected.

THALLUS crustose, areolate, poorly developed or absent, usually confined to the apothecia, 0.1–0.2 mm diam., orange to deep orange [RAL 2011]. CORTEX paraplectenchymatous, 12.9–67.1 µm high, composed of thin-walled cells, (2.38–)4.8–7.4(–10.5) µm diam. ALGAL LAYER ± continuous, 49.5–97.9 µm thick. MEDULLA loosely interwoven by thin-walled hyphae under the apothecia, 59.8–86.1 µm high.

APOTHECIA lecanorine to zeorine, numerous, adnate, always aggregated (2–7) or crowded together, disc margins present, smooth, entire, concolorous with thallus, sun yellow [RAL 1037] to deep orange

[RAL 2011], disc round to irregular, yellow-orange [RAL 2000] to signal orange [RAL 2010], flat to concave, 0.3–0.7 mm diam. Exciple 9.6–14.8 µm thick, consisting of 2–4 layers of cells, upper part of cells spherical, 3.2–6.0 µm diam, cells of lower part elongated, 3.5–10.6 × 1.4–3.6 µm. Hypothecium thin, 22.3–34.7 µm high, composed of several lines of paraplectenchymatous cells, 2.9–5.2 × 2.3–4.6 µm. Hymenium 52.2–89.5 µm high, colorless. Paraphyses anastomosed, generally dichotomously branched or trigeminally branched at tips, the 3–4 terminal cells gradually enlarging towards tips, the widened cells nonuniform in size, the second cells 3.5–6.7 µm diam., and the third ones 3.2–5.3 µm diam.

Asci teloschistes-type, 8-spored. Ascospores colorless, ellipsoid, (11.2–)11.7–17.5(–4.7) × 5.8–8.4(–9.3) µm, septum 3.3–6.5 µm diam.

Spot tests—K+ red.

Chemistry—Parietin, emodin, and two unknown anthraquinones.

Ecology—*Filsoniana lhasanensis* grows on rocks in open areas and associates with species of *Aspicilia, Lecanora, Rusavskia, Physcia, Rinodina, Rhizoplaca,* and *Acarospora*. The new lichen is distributed in arid or semiarid areas of Lhasa city and Shannan city at elevations of 4200–4432 m.

Additional specimen examined: **CHINA. Tibet**, **Shannan City**, Nagarze county, Yamzho Yumco, 29°09′34″N 90°30′19″E, alt. 4432 m, 10 September 2011, X.M. Wen 20110910–05 (XZ; GenBank MK153161, MK439835, MK439831).

Remarks: *Filsoniana lhasanensis* is characterized by a reduced, dark orange to brownish orange thallus and aggregated apothecia. It is morphologically similar to *Xanthocarpia ferrarii* (Bagl.) Frödén & al., which differs by its narrower septum, larger ascospores, well developed true exciple, zeorine to biatorine apothecia, and classification in *Xanthorioideae* (Arup & al. 2013).

Filsoniana australiensis, F. rexfilsonii, and *F. lhasanensis* have similar paraplectenchymatous cortex and broad paraphyses (Kondratyuk & al. 2007). However, *F. australiensis* and *F. rexfilsonii* have well-developed thalli (*F. australiensis* has a placodioid thallus, and *F. rexfilsonii* has a squamulose thallus) with scattered or rare apothecia, whereas *F. lhasanensis* has a poorly developed thallus consisting of only a few scattered areoles.

A summary of the characteristics of *F. lhasanensis* and morphologically similar species is provided in Table 3.

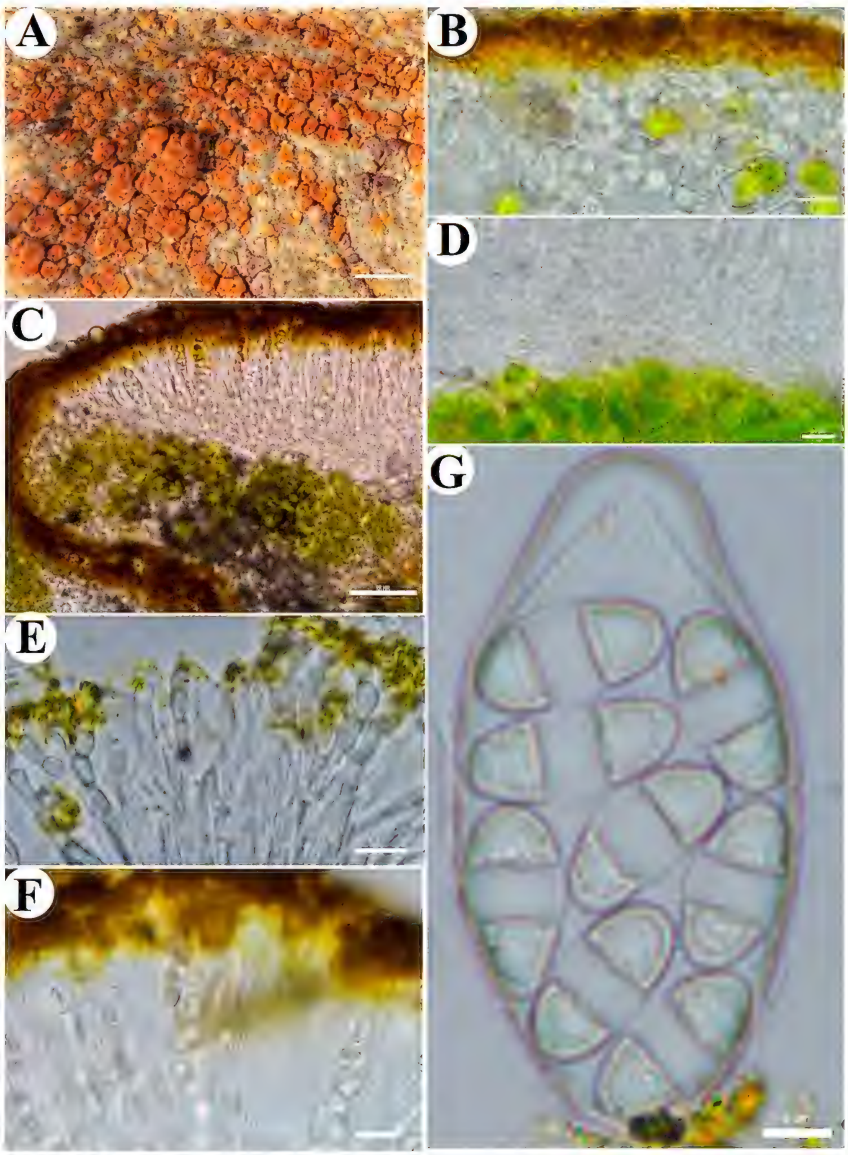

Fig. 2. ***Filsoniana lhasanensis*** (XZ (Wen 20110901–29)): A. Thallus and apothecia; B. Cortex of thallus; C. Cross section of the apothecium; D. Hypothecium; E. Paraphyses branched and enlarged at the tips; F. Paraphyses branched and anastomosed; G. Ascus containing eight ascospores. Scale bars: A = 1 mm; B–F = 10 μm; G = 5 μm.

TABLE 3. Comparison of *Filsoniana lhasanensis* with morphologically similar species of *Filsoniana*, *Thelliana*, and *Xanthocarpia*

CHARACTER	*F. australiensis*	*F. rexfilsonii*	*X. ferrarii*	*T. pseudokiamae*	***F. lhasanensis***
Thallus	Well developed, placodioid, distinctly lobate, dull pink to dirty brownish pink	Well developed, squamulose, brownish orange	Absent or poorly developed, pale gray	Margins, brownish yellow, with rare brighter yellow blastidia or punctiform sorelia	Absent or poorly developed, usually restricted around apothecia, orange to deep orange
Apothecia	Mainly lecanorine, sometimes zeorine, immersed in papillae to sessile, disc concave, reddish orange	Zeorine, margin slightly raised, disc dark orange	Common, zeorine to biatorine, orange to dark orange	Biatorine, rare, disc & proper margin reddish orange	Lecanorine to zeorine, numerous, adnate, aggregated, disc yellow-orange to signal orange
Paraphyses	Rather wide, simple, apical cell 4–5 µm	Apically widened, apical cells 6–7 µm, with oil droplets	Simple to branched, apical cells 4–5 µm	Not observed	Anastomosed, tips branching, the 3–4 terminal cells gradually enlarged towards the tips
Ascospores	10–13 × 6–8 µm	16–20 × 6.5–7 µm	17–23 × 5.5–7.5 µm	Not seen	11.7 –17.5 × 5.8–8.4 µm
Septal diam.	4–6 µm	2–5 µm	1–2 µm	Not observed	3.3–6.5 µm.
Ecology	Exposed rocks	In sheltered or exposed situations, on various rocks	Rocks	Rock surfaces or in rock crevices	Rocks in open areas
Distribution	Australia	Australia	Europe–central Asia	Australia	China

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Sarcopodium flocculentum, the correct name for *S. macalpinei*

Shaun R. Pennycook[1*] & Paul M. Kirk[2]

[1] *Manaaki Whenua – Landcare Research*
Private Bag 92170, Auckland 1072, New Zealand

[2] *Royal Botanic Gardens*
Kew, Surrey, TW9 3DS, UK

[*] Correspondence to: *PennycookS@LandcareResearch.co.nz*

Abstract—The nomenclatural background of the species treated as *Sarcopodium macalpinei* is briefly outlined, and the requirement to supersede that name with a combination based on *Nectriella flocculenta* [≡ *Lanatonectria flocculenta*] is explained.

Key words—*Actinostilbe flocculenta, Actinostilbe macalpinei, Kutilakesopsis macalpinei,* ICN, code-compliance

In a morphological study, Sutton (1981) synonymised *Actinostilbe* Petch and *Kutilakesopsis* Agnihothr. & G.C.S. Barua with the earlier genus *Sarcopodium* Ehrenb. and published a new combination *Sarcopodium macalpinei* for the type of *Kutilakesopsis*.

Rossman & al. (1999) proposed *Lanatonectria* Samuels & Rossman, typified by a sexual morph for which they published the new combination *L. flocculenta*, additionally proposing a new combination *Actinostilbe macalpinei* for the conspecific asexual morph.

In a multi-gene analysis, Lombard & al. (2015) included sequences from the type species of *Sarcopodium* (*S. circinatum*), *Actinostilbe* (*A. vanillae* ≡ *S. vanillae*), and *Kutilakesopsis* (*K. macalpinei* ≡ *S. macalpinei*), demonstrating that they were all included within a monophyletic *Sarcopodium* clade, thereby confirming the synonymy of these three genera. They also included

Lanatonectria as a synonym based on the established synonymy of its type (*L. flocculenta*) with *Sarcopodium macalpinei;* consequently, they recombined four of the five *Lanatonectria* species in *Sarcopodium* but did not recombine *L. flocculenta* (presumably because of its existing heterotypic *Sarcopodium* synonym).

Rossman & al. (2016) recommended *Sarcopodium* as the accepted generic name in preference to *Lanatonectria* and *Actinostilbe,* a decision based on priority, widespread use, and the greater number of existing names; but they continued to cite *L. flocculenta* as *S. macalpinei.*

However, *Sarcopodium macalpinei* is not the correct name for this species, since it fails to use the epithet of the earliest available legitimate name, as required by ICN (Shenzhen) Art. 11.4 (Turland & al. 2018). The correct name has been proposed by Pennycook & Kirk (2019):

Sarcopodium flocculentum (Henn. & E. Nyman) Pennycook & P.M. Kirk, Index Fungorum no. 418: 1. 2019
≡ *Nectriella flocculenta* Henn. & E. Nyman, Monsunia 1: 160. 1899 ["1900"]
≡ *Nectria flocculenta* (Henn. & E. Nyman) Höhn., Sitzungsber. Kaiserl. Akad. Wiss., Wien, Math.-Naturwiss. Cl., Abt. 1, 121: 360. 1912
≡ *Lanatonectria flocculenta* (Henn. & E. Nyman) Samuels & Rossman, Stud. Mycol. 42: 138. 1999
≡ *Actinostilbe flocculenta* (Henn. & E. Nyman) Rossman, Samuels & Seifert, IMA Fungus 4(1): 46. 2013
= *Kutilakesopsis macalpinei* Agnihothr. & G.C.S. Barua, J. Indian Bot. Soc. 36: 309. 1957 [as '*macalpineae*']
≡ *Sarcopodium macalpinei* (Agnihothr. & G.C.S. Barua) B. Sutton, Trans. Brit. Mycol. Soc. 76: 99. 1981
≡ *Actinostilbe macalpinei* (Agnihothr. & G.C.S. Barua) Seifert & Samuels, Stud. Mycol. 42: 138. 1999

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Pteridicolous ascomycetes from a cloud forest in eastern Mexico

Rosario Medel-Ortiz[1*], Yajaira Baeza[2], & Francisco G. Lorea-Hernández[3]

[1]*Centro de Investigación en Micología Aplicada, Universidad Veracruzana, Médicos No. 5, Col. Unidad del Bosque, 91010, Xalapa, Veracruz, México.*

[2]*Facultad de Agronomía, Universidad Veracruzana, Zona Universitaria, 91000, Xalapa, Veracruz, México*

[3]*Instituto de Ecología, A.C. Red de Sistemática y Biodiversidad, Carretera antigua a Coatepec 351, 91070, Xalapa, Veracruz, México.*

[*] Correspondence to: *romedel@uv.mx*

Abstract—Twenty-one ascomycetous taxa collected on ferns in a cloud forest of Veracruz, Mexico are reported and described. Fourteen represent new records for the Mexican mycobiota: *Bisporella pteridicola*, *Crocicreas quinqueseptatum*, *Dasyscyphella dryina, Durella macrospora, Hamatocanthoscypha helicotricha, Hyaloscypha fuckelii*, *Lachnum brevipilosum*, *L. nudipes*, *Mollisia ventosa, Orbilia auricolor, Protocreopsis pertusa, Seimatosporium tostum*, *Stictis carnea*, and *S. radiata*. Two collections—*Cyathicula* and cf. *Arachnopeziza*—that could not be fully identified may represent new species. The remaining five taxa have previous Mexican records but are reported here from new fern hosts. This study increases to 25 the number of ascomycete species known to occur on ferns in the cloud forests of Mexico.

Key words—*Cyatheaceae, Helotiales, Hypocreales, Ostropales, Xylariales*

Introduction

The *Ascomycota*, with around 90,000 species (Cannon & al. 2018), is the most diverse group in kingdom *Fungi*. Its diversity significantly complicates gaining knowledge of individual species, especially those with minute fruitbodies restricted to specialized substrates. Such is the case of fungi growing on ferns. Most fungi reported on ferns are saprobes, a group that

receives less attention than parasites (Mehltreter et al. 2010). Currently 69 ascomycete species have been recorded in cloud forest of Veracruz (Medel 2013), small in comparison to the over 500 fern species known to inhabit cloud forests (Tejero-Díez & al. 2011). Although the first fern-related fungal study was devoted to rust fungi (Stevenson 1945), subsequent studies have been more focused on ascomycetes and their anamorphs (e.g., *Mycosphaerellaceae* and *Periconiella;* Braun 2004, Kirschner & Liu 2014). Other studies have centered on endophytic ascomycetes and fern-associated saprobes (Cannon 1997, Castañeda-Ruiz & Heredia 2000, Del Olmo & Arnolds 2014, Dingley 1972, Medel & Lorea-Hernández 2008, Samuels & Rogerson 1990).

For Mexico there are relatively few studies on the diversity of fern-inhabiting fungi (Castañeda-Ruiz & Heredia 2000, Haines 1980, Medel & Lorea-Hernández 2008, Medel & al. 2010, Samuels & Rogerson 1990). So far, the seven ascomycete species recorded growing on ferns represent only three genera: *Crocicreas* Fr. (1), *Dimeriella* Speg. (1), and *Lachnum* Retz. (5). The few *Ascomycota* recorded from these forests contrasting with the great diversity of fern species suggests a high diversity yet to be explored. The present study was conducted in order to provide more information about the diversity of fern-inhabiting fungi in Mexican cloud forests.

Materials & methods

Sampling sites in central Veracruz state (eastern Mexico) were selected based on the high fern diversity within an area. Three sampling sites were chosen: El Riachuelo, Los Encinales, and Río Xocoyolapan. Field work was conducted during August–November 2011. Fungi were collected by opportunistic sampling of different fern species, with fronds and rachises presenting ascomata or stromata selected and placed in paper bags (Mueller & al. 2004).

Fruiting bodies were identified and processed following standard mycological techniques for *Ascomycota* (Dennis 1978). Specimens were hand sectioned, pretreated with 3% aqueous KOH, and stained with phloxine and Melzer's reagent; ascal tip bluing reactions are designated by J– (negative, no blue present) and J+ (positive, blue present). Tissues were examined microscopically using a Zeiss Primo Star microscope. Averages, ranges, and Q-calculations (Largent & al. 1977) are based on 30 measurements. Colours are coded according to Kornerup & Wanscher (1978). Ascomata were photographed digitally with a Sony Cyber-Shot camera mounted on a Zeiss Stemi DV4 stereomicroscope. The specimens were identified using specialized literature (Breitenbach & Kränzlin 1984, Carpenter 1981, Dennis 1949, 1956, 1960, 1978). Fungal nomenclature follows Index Fungorum (2019), and host plants were identified following Mickel & Smith (2004). All specimens are

deposited in the mycological collection of the Herbarium, Instituto de Ecología A.C. (XAL). Specimens discovered in XAL and also examined are noted as "additional specimens examined" in species descriptions where pertinent.

Taxonomy

cf. *Arachnopeziza* Figs 1–3

Apothecia sessile, cup-shaped, reddish-golden (6C7) to Pompeian yellow (5C6), ≤1 mm diam., margin hairy (sparsely pilose), hairs white (1A1), readily dropping from the margin to give a smooth appearance. Subiculum white to pale yellowish white (1A1, 2A1), not scattered on the substrate, reticulate or net-like, with hyphae 2–3 µm diam., septate, hyaline, thick-walled (≤1 µm). Asci cylindrical, 70–90(–100) × 7–9(–10) µm, thin-walled, hyaline, 1–2-seriate, pore J+. Ascospores cylindrical-ellipsoid, (13–)14–15 × 5 µm (Q = 2.8), smooth, hyaline, 0–1-septate, biguttulate, with sheath and hyaline appendages observed in Cresyl blue. Paraphyses filiform, 1–2 µm diam., hyaline, septate toward the base. Ectal Excipulum a textura globulosa to textura angularis, cells 12–25(–40) µm diam.

Habitat—Gregarious, on rachises of *Alsophila firma*. Known only from these collections.

Specimens examined—**MEXICO. Veracruz: San Andrés Tlalnelhuayocan County**, Río Xocoyolapan, 19°30.89′N 97°00.39′W, 1590 m, 13 October 2011, Córdova 78.

Additional specimens examined: **MEXICO. Veracruz: San Andrés Tlalnelhuayocan County**, Rancho Agüita Fría, 6 April 2007, Medel 1362; 1363-A.

Arachnopeziza Fuckel is characterized by small apothecia growing on a densely reticulate, net-like subiculum covered by hairs, and ellipsoid-fusoid to filiform, 1–7-septate ascospores (Korf 1951). The genus has a worldwide temperate distribution but is uncommon in the tropics (Gamundí & Giaiotti 1994). Although the studied specimens suggest an affinity with *Arachnopezizaceae,* they do not match any known genus or species covered in the references consulted (Dennis 1949, Huhtinen 1987, Korf 1951). The 0–1-septate spores covered by a hyaline sheath with a small appendage resemble those of *Arachnopeziza aurelia* (Pers.) Fuckel, which differs in its long hairs, slightly larger spores (17–22 × 3.5–5.5 µm, 0–3-septate; Korf 1951). The presence on the apothecial margin of very thick, scarce, and septate hairs that drop off, leaving a smooth margin (as in our specimen; Fig. 1) is a feature unknown in *Arachnopeziza.* The subiculum is restricted to the apothecial base and not distributed throughout the substrate, unusual in *Arachnopeziza* (Seaver 1938), but not uncommon in *Parachnopeziza* Korf.

In *Parachnopeziza,* however, apothecia grow directly from a small stipe immersed in the substrate (Korf 1978) growing directly from a subiculum, as occurs in *Arachnopeziza*, and certainly in our specimen.

Bisporella pteridicola F. Ren & W.Y. Zhuang,
Mycosystema 36 (4): 408 (2017). Figs 4, 5

Apothecia superficial, cup-shaped to discoid. Disc concave, yellow (4A6), pastel yellow (2A4), or chicken yellow (2A6), translucent, waxy in appearance, 0.2–0.4 mm diam. Stipe short or absent, concolorous with the disc. Asci claviform (32–)35–40(–45) × 5–6 µm, 8-spored, biseriate, apical pore J–, arising from croziers. Ascospores fusiform (5 –)8–9(–10) × 2–3 µm (Q = 4.3), hyaline, with two oil drops and one septum visible in KOH. Paraphyses filiform, slightly enlarged at the apex, 1.5–2 µm diam. Ectal Excipulum a textura angularis, gelatinized, 15–40 µm thick, cells 3–6 µm diam., protruding from outer surface ≤3 µm. Medullary Excipulum a textura intricata, thin, hyaline, not gelatinized, cells 2–3 µm diam.

Habitat—On rachises of unidentified fern as well as on fern rachises and leaf blades of *Alsophila firma, Cyathea bicrenata*, *Sphaeropteris horrida*, *Pecluma alfredii*, and *Thelypteris* sp.

Specimens examined—**MEXICO. Veracruz: San Andrés Tlalnelhuayocan County, Río Xocoyolapan,** 19°30.89′N 97°00.39′W, 1590 m, 13 October 2011, Córdova 80c; 4 November 2011, Castillo del Moral 63, 66; 8 December 2011, Medel & Lorea 2203. El Riachuelo; 19°30.99′N 97°00.39′W, 1626 m, 18 August 2011, Baeza 47a, Córdova 67, 71; 11 November 2011, Medel 2192. Los Encinales, 19°31.10′N 97°00.32′W, 1630 m, 10 August 2011, Baeza 36; 18 August 2011, Baeza 49,55, 57; Medel & Lorea 2158, Córdova 73, 74.

Bisporella Sacc. is a genus easily recognized by its small sessile bright yellow apothecia growing on woody substrata (Carpenter & Dumont 1978a, Dumont 1981). *Bisporella pteridicola* was described growing on ferns in Asia (Zhuang & al. 2017). Ours is the first report of the species from Mexico. Our collections agree with the description in Zhuang & al. (2017) in color, size, and shape of the apothecia, ascospore measurements, and ecology (growth on ferns).

Coenogonium botryosum C. Knight,
Syn. Queensl. Fl. 1(Suppl.): 74 (1886). Figs 6, 7

Apothecia superficial, discoid, sessile, flattened, 0.5–1 mm diam., pale yellow (3A3), waxy in appearance, margin differentiated from the disc, smooth, yellowish white (3A2), paler than the disc. Thallus filamentous or felt-like and pilose, with short, upright algal threads resembling hairs,

greyish yellow to linden green (2B5-2C5). Hymenium J+. Hairs small and thin, linden green (2C5) to pale yellow (1A3-2A3), filiform, septate. Asci cylindric-clavate (48–)50–55(–60) × 4–5 µm, thin walled, uniseriate. Ascospores ellipsoid (7–)8–9(–12) × 2 µm (Q = 4.2), hyaline, smooth, 0–1-septate, with 4 small guttules. Paraphyses cylindrical, apices 4–5 µm diam., bifurcate, hyaline, septate. Ectal excipulum a textura globulosa, with hyaline cells.

Habitat—Gregarious, on fronds of *Adiantum andicola* and *Grammitis* sp.

Specimens examined—**MEXICO. Veracruz: San Andrés Tlalnelhuayocan County**, El Riachuelo, 19°30.99′N 97°00.39′W, 1626 m, 8 December 2011, Baeza 70, Medel & Lorea 2211, 2215.

Coenogonium Ehrenb. is a tropical and subtropical ascolichen genus found on all continents (GBIF 2019, Rivas-Plata & al. 2006, Uyenco 1963). The filamentous green-pale yellowish thallus attached to the substrate by small filaments as well as the threadlike algae, absence of septa, uniseriate asci, and paraphyses with capitate subglobose apices are characteristic of *C. botryosum* (Rivas-Plata & al. 2006). Two similar species are *C. moniliforme* Tuck., which has moniliform algae without septa, and *C. implexum* Nyl., which has bright yellow thalli and a cottony texture.

Known from Neotropics and eastern Paleotropics (GBIF 2019, Rivas-Plata & al, 2006, Uyenco 1963), *Coenogonium botryosum* was reported previously for Veracruz, Mexico, growing on *Ficus* (Uyenco 1963); this is the first report of the species on ferns.

Crocicreas quinqueseptatum S.E. Carp.,
Mem. New York Bot. Gard. 33: 160 (1981). Figs 11, 12

Apothecia cup-shaped, 0.5–0.8 mm diam. Disc white to yellowish white (2A2, 2A1). Margin denticulate, inrolled over the hymenium when dry, almost hyaline or translucent with long teeth; teeth fragile, formed by groups of long, septate, hyaline hyphae, 100–115(–400 µm) × 40–48 µm, lighter in colour than the rest of the apothecium, white to yellowish white (2A1-2A2), 8–12 teeth per apothecium; breaking easily leaving the apothecia non-denticulate. Stipe cylindrical, thin, concolorous with apothecia. Asci cylindrical, tapering toward the base, (60–)80–105 × 6–8 µm, thin-walled, apical pore J+, biseriate, base without croziers. Ascospores fusoid to fusiform with subacute to acute ends, smooth, (20–)26–30 × 3–4 µm (Q = 5.5), 5-septate (rarely 6–7), hyaline. Paraphyses filiform, unbranched,

1–2 µm diam., hyaline. Ectal excipulum single layered, gelatinous, composed of long cells in the inner part, extending outward from the disc to form the teeth. Medullary excipulum not differentiated.

Habitat—On fallen stems and rachises of *Alsophila firma* and *Cyathea bicrenata.*

Specimen examined—**MEXICO. Veracruz: San Andrés Tlalnelhuayocan County,** Los Encinales, 19°31.10′N 97°00.32′W, 1630 m, 10 August 2011, Medel & Lorea 2168.

Crocicreas quinqueseptatum was described by Carpenter (1981) as having ascospores with a variable number (4–7) of septa and which are slightly longer and narrower [(28–)30–33(–35) × (2–)2.5–3 µm] than those found in our specimen. Other features (outer apothecial surface, morphology, and measurements) are close to *C. helios* var. *parahelios* S. E. Carp., which differs by 0–3-septate ascospores, an absent or poorly developed medullary excipulum, and broader apothecia (≤1.5 mm; Carpenter 1981). *Crocicreas quinqueseptatum* has been reported growing on angiosperm stems, especially fallen herbaceous stems of *Asteraceae* in South America. This is the first report of this species on ferns.

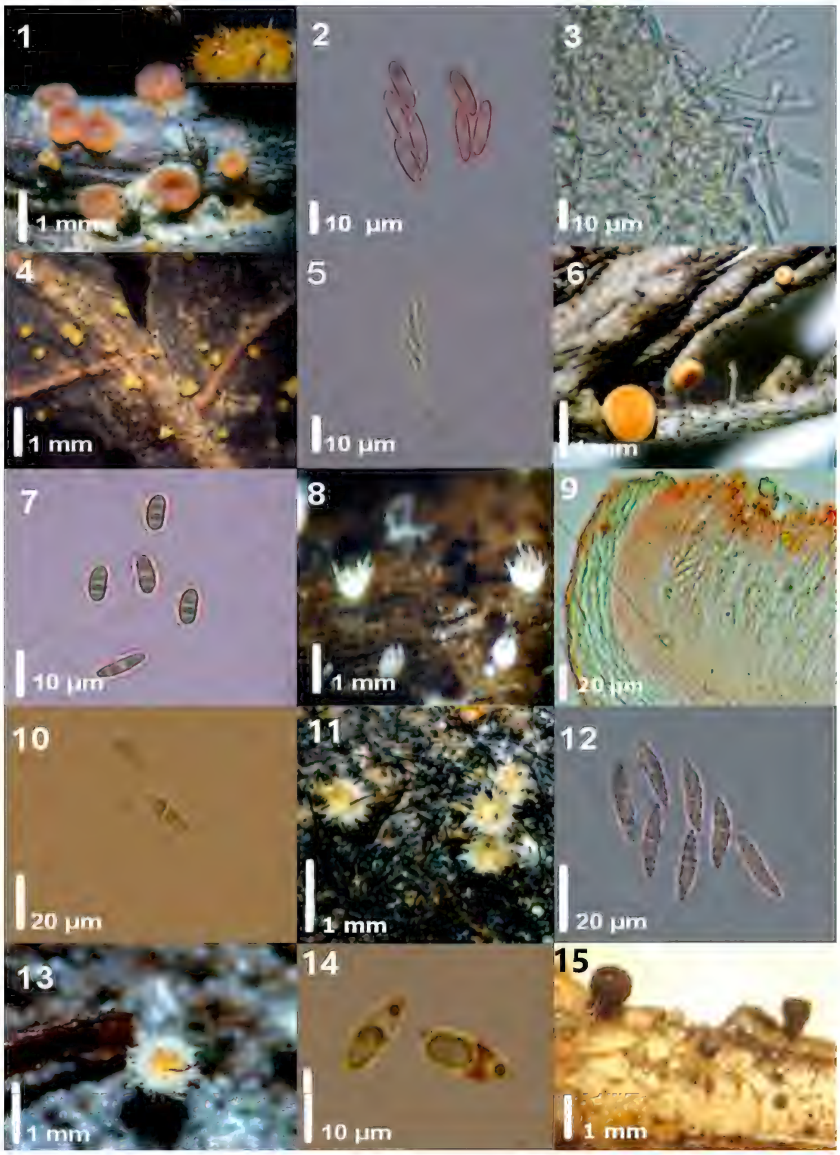
***Cyathicula* sp.** Figs 8–10

Apothecia cup-shaped, sessile, disc flattened or concave, ≤1 mm diam., pastel yellow (3A4); margin dentate with 6–10 hyaline teeth per ascoma, teeth composed of groups of long, hyaline, aseptate hyphae that extend beyond the margin, each tooth separated by c. 420–480 µm. Asci cylindric-clavate, (96–)110–140 × (7–9)10–11 µm, 8-spored, biseriate, apical pore J–. Ascospores ellipsoidal-fusiform, 13–16 × 5–6 µm (Q = 2.6), smooth, hyaline, 1–3-septate, guttulate. Paraphyses filiform, apices simple or branched, 2–3 µm diam. at apex, septate; embedded with asci in a gelatinous matrix and separated only with difficulty. Ectal excipulum a textura prismatica to textura porrecta, hyphae single-layered, long-celled, subparallel, close together, thick-walled, hyaline, smooth, lacking crystals. Medullar excipulum little differentiated, hyphae 3–5 µm diam., not easily observed due to gelatinous consistency.

Habitat—On rachises of *Cyathea bicrenata.* Known only from our collections.

Specimens examined—**MEXICO. Veracruz: San Andrés Tlalnelhuayocan County;** El Riachuelo, 19°30.99′N 97°00.39′W, 1626 m, 4 November 2011, *Baeza 56;* Los Encinales, 19°31.10′N 97°00.32′W, 1630 m, 13 October 2011, Baeza 56a; 4 November 2011, Baeza 61, Castillo del Moral 64.

We place our material into *Cyathicula* based on its cupulate, sessile apothecium with a toothed margin, whitish yellowish to pale brown color,



Figs 1–15. **cf.** ***Arachnopeziza.*** 1. Apothecia showing scarce subiculum and hairs (top right); 2. Ascospores in Congo red; 3. Excipulum showing hyphae from the subiculum. ***Bisporella pteridicola.*** 4. Apothecia; 5. Asci with ascospores. ***Coenogonium botryosum.*** 6. Apothecia; 7. Ascospores. ***Cyathicula*** **sp.**; 8. Apothecia; 9. Cross section of excipulum, 10. One-septate ascospores. ***Crocicreas quinqueseptatum.*** 11. Apothecia showing dentate margin; 12. Ascospores. ***Dasyscyphella dryina.*** 13. Apothecium; 14. Ascospores. ***Durella macrospora.*** 15. Apothecia.

septate ascospores, J– asci, and the presence of a gelatinous matrix (Carpenter & Dumont 1978b). Nonetheless, we must also note that the specimens fit diagnostic characters of *Crocicreas* (Carpenter 1981). The controversy over whether *Crocicreas* and *Cyathicula* are congeneric has lasted for decades (Iturriaga & al. 1999, Zheng & Zhuang 2016). According to one classification of *Helotiales* (Baral & al. 2015), *Crocicreas* is restricted only to the type species *C. gramineum* (Fr.) Fr., and *Cyathicula* is unrelated. Although Wijayawardene & al. (2018) support this distinction, we agree with the conclusion of Zheng & Zhuang (2016) that existing data are insufficient for determining the relationship between *Crocicreas* and *Cyathicula*. Molecular analysis is still needed for us to assign our material definitively to a genus.

Dasyscyphella dryina (P. Karst.) Raitv.,
Akad. Nauk Estonskoi S.S.R., Inst. Zool. Bot., Tartu: 72 (1970). Figs 13, 14

Apothecia superficial, cup-shaped, stipitate, covered with white (1A1) hairs. Disc 0.8–1 mm diam., yellowish white (2A2) to pale yellow (2A3), smooth. Stipe cylindrical, covered with white (1A1) hairs with small hyaline crystals at the tips. Hairs cylindrical, septate, slightly granular, hyaline, easily visible, giving a distinctive villous appearance to the apothecium. Asci cylindrical, 45–50 × 3–4 µm, hyaline, 8-spored, irregularly biseriate, thin walled, apical pore J+. Ascospores cylindric-ellipsoid to fusoid, (6–)7–10 × 2–3 µm, (Q = 4.2), smooth, hyaline, with rounded ends. Paraphyses filiform, slightly lanceolate, 1 µm diam., hyaline, projecting beyond the asci by 10–20 µm.

Habitat—On rachises of *Alsophila firma*.

Specimens examined—**MEXICO. Veracruz: San Andrés Tlalnelhuayocan County**, Río Xocoyolapan, 19°30.89′N 97°00.39′W, 1590 m, 19 August 2011, Medel 2180, Medel 2181.

The studied specimen matches well with the concept of *Lachnum distinguendum* sensu Dennis (1949, 1956, 1960), which is a synonym of *Dasyscyphella dryina*. Dennis (1956) cited spores 2 µm longer than those of our collections, and filiform paraphyses which agreed with our specimen. Rick (1906) described *L. distinguendum* Rick with broader apothecia (≤2 mm diam.), larger asci (50–69 × 7–10 µm), larger ascospores (10–15 × 3–4 µm), and lanceolate paraphyses (3–4 µm diam.). Raitviir (1970) cited slightly longer ascospores (9–12 × 2–3.2 µm) and cylindrical paraphyses with pointed tips. Nonetheless, our collection fits better Dennis's concept, because our material has paraphyses that exceed the asci, while Raitviir (2002) described paraphyses not exceeding the asci.

Dasyscyphella dryina is known from Europe and South America on *Betula, Fagus,* and *Populus* (Dennis 1949, 1956. 1960, Raitviir 1970, Rick 1906).

Durella macrospora Fuckel,
Jahrb. Nassauischen Vereins Naturk. 23–24: 281 (1870). Figs 15–17

Apothecia superficial, cup-shaped, stipe short with a wide base. Disc flat, 0.2–0.5 mm diam., wrinkled, brownish gray (10F2) with dark brown (7F8) tones, hard consistency. Asci cylindrical (90–)100–130 × 11–12 µm, hyaline, 8-spored, irregularly biseriate, apical pore J–. Ascospores ellipsoid-fusiform, (18–)19–22(–23) × 4–5 µm (Q = 4.2), smooth, hyaline, 3-septate, constrained at the septum, ends rounded, with 4 small guttules. Paraphyses cylindrical, slightly wider at the apex (c. 3 µm) brownish to reddish brown in KOH. Ectal excipulum of parallel brown hyphae.

Habitat—On fronds of *Sticherus palmatus.*

Specimen examined—**MEXICO. Veracruz: San Andrés Tlalnelhuayocan County,** El Riachuelo, 19°30.99′N 97°00.39′W, 1626 m, 8 December 2011, Medel 2210.

Spores of *Durella macrospora* have been cited as 15–21 × 3–5.5 µm (Breitenbach & Kränzlin 1984, Medardi 2004). Although the spores in our collection are 2 µm longer, other morphological characters (black apothecia, hard consistency, ectal excipulum of parallel brown hyphae) agree well with the published descriptions (Breitenbach & Kränzlin 1984, Medardi 2004).

Durella macrospora has been previously recorded growing on wood of deciduous trees such as *Fagus*, *Malus domestica,* and *Quercus* sp. (Breitenbach & Kränzlin 1981, Medardi 2004), but not on ferns. Previously known only from Europe (Breitenbach & Kränzlin 1984, Dennis 1956, Medardi 2004).

Hamatocanthoscypha helicotricha Huhtinen,
Karstenia 29(2): 182 (1990 ["1989"]). Figs 18–20

Apothecia cup-shaped, disc concave, pale yellow (3A3) to pastel yellow (3A4) shades, 0.5 mm diam., covered with fine, white (1A1) to yellowish white (2A1-2A2) short hairs. Stipe cylindrical, short, slightly robust, concolorous with apothecia. Hairs cylindrical, apically coiled to uncinate, 12–32 × 2–4 µm, the apex tapering to ≤1 µm diam., hyaline, septate toward to the base, smooth. Asci cylindric-clavate, apex conical, base attenuate, (42–)45–72 × 6–7 µm, hyaline, pore J–, 8-spored, biseriate, base with croziers. Ascospores ellipsoid-fusoid, hyaline, smooth, 7–9(–10) × 2–3 µm (Q = 2.6), 1-septate, biguttulate. Paraphyses filiform, 2 µm diam., narrowing toward the base.

Habitat—On rachises of *Cyathea bicrenata* and fronds of *Sticherus palmatus*.

Specimens examined—**MEXICO. Veracruz: San Andrés Tlalnelhuayocan County**, El Riachuelo, 19°30.99′N 97°00.39′W, 1626 m, 8 December 2011, Medel & Lorea 2213. Los Encinales, 19°31.10′N 97°00.32′W, 1630 m, 10 August 2011, Baeza 41.

Huhtinen (1990) and Raitviir (2004) report somewhat larger (9.8–12.8 × 2.8–4 µm) spores than found in our specimens, but the presence of strongly coiled hairs at the apex distinguishes this species. *Hamatocanthoscypha helicotricha* has been recorded on fern rachises from Colombia and Cuba (Huhtinen 1990, Raitviir 2004); this is the first report of the species for Mexico.

Hyaloscypha fuckelii Nannf.,
Nova Acta Regiae Soc. Sci. Upsal., Ser. 4, 8(2): 273 (1932). Figs 21, 22

Apothecium superficial, sessile, cup-shaped. Disc concave, 0.1–0.3 mm diam., white (1A1), translucent when fresh or when rehydrated in KOH. Receptacle with fine, whitish hairs. Hairs filiform, cylindrical, curved in the apex, thin-walled, slightly granular. Asci clavate, 50–66(–67) × 4–5 µm, hyaline, thin-walled, 8-spored, irregularly biseriate, apical pore J+, base with croziers. Ascospores ellipsoid, (5–)6–8(–10) × 2 µm, (Q = 3.2), 0–1-septate, smooth, hyaline, with small oil drops. Paraphyses filiform, protruding ≤9 µm beyond asci, narrow, smooth, hyaline, apical cell with small guttules.

Habitat—On rachises of *Alsophila firma*.

Specimen examined—**MEXICO. Veracruz: San Andrés Tlalnelhuayocan County**, El Riachuelo, 19°30.99′N 97°00.39′W, 1626 m,10 August 2011, Baeza 38.

Our collection agreed with *Hyaloscypha fuckelii* as described by Huhtinen (1990). The similar *H. albohyalina* (P. Karst.) Boud. differs in its narrow hairs and smaller spores.

Hyaloscypha fuckelii is widely distributed in Europe and North America (Huhtinen 1990) and has been reported growing on monocotyledonous genera such as *Juncus*, *Typha,* and *Molinia*. This is a new record for Mexico and the first report on ferns.

Lachnum brevipilosum Baral,
Beih. Z. Mykol. 6: 74 (1985). Figs 23, 24

Apothecium superficial, cup-shaped. Disc concave, white (1A1) to pale (2A2), 0.8–1 mm diam. Receptacle covered with whitish hairs visible

to the naked eye. Stipe cylindrical, 0.6 mm long, covered by hairs generally concolorous with disc (white, 1A1) except for some with a yellowish gray (4B2) base. Hairs cylindrical, 130–150 × 4–5 µm (the apex tapering to ≤2–3 µm), 5–7-septate, hyaline, covered by granules. Asci clavate-cylindrical, 42–50 × 4–5 µm, hyaline, pore J+, 8-spored, biseriate, croziers not observed. Ascospores ellipsoid, smooth, with rounded ends, 8–10(–12) × 2 µm (Q 4.2), hyaline, 1-septate, biguttulate. Paraphyses filiform, septate, protruding by 5–10 µm above the asci, hyaline.

Habitat—On rachises of *Alsophila firma* and *Cyathea bicrenata.*

Specimens examined—**MEXICO. Veracruz: San Andrés Tlalnelhuayocan County**, Río Xocoyolapan, 19°30.89′N 97°00.39′W, 1590 m, 4 November 2011, Baeza 58. Paraje El Riachuelo, 19°30.99′N 97°00.39′W, 1626 m, 4 November 2011, Córdova 86.

The Mexican specimens agree with the morphology of *Lachnum brevipilosum* as provided by Dennis (1949, as *Dasyscyphus brevipilus* Le Gal) and Ye & al. (2006), except for the length and width of the hair apices.

Lachnum brevipilosum has been reported growing on stems of *Clematis, Fagus*, and *Rubus* from Europe and temperate China (Dennis 1949, Ye & al. 2006) This is a new record for Mexico and represents the first report on ferns.

Lachnum nudipes (Fuckel) Nannf.,
Svensk Bot. Tidskr. 22: 124 (1928). Figs 25, 26

Apothecium superficial, cup shaped. Disc concave slightly flattened, yellowish white (4A2) to pale yellow (4A3), 0.3–0.4 mm in diameter. Receptacle densely covered with white (1A1) hairs. Stipe cylindrical, with whitish hairs (1A1), more or less equal to the diameter of the disc. Hairs cylindrical, ornamented with granules, widening at apex to 3–4 µm, longer than 80 µm, hyaline in KOH. Asci clavate, (35–)38–47 × 4–5 µm, 8-spored, biseriate, pore J+, base without croziers. Ascospores fusiform to elliptical with rounded ends, (5–)6–8(–9) × 1–2(–3) µm (Q = 3.1), smooth, hyaline. Paraphyses lanceolate, septate towards the base, (50–)68–70 × 3–4 µm, clearly extending beyond the asci.

Habitat—On fronds of *Lophosoria quadripinnata.*

Specimens examined—**MEXICO. Veracruz: San Andrés Tlalnelhuayocan County**, Río Xocoyolapan 19°30.89′N 97°00.39′W, 1500 m, 18 August 2011, Córdova 72, 13 October 2011, Baeza 51; 4 November 2011, Córdova 65, 84, Castillo del Moral 65.

Our material agrees with Dennis's (1949) descriptions of *Dasyscypha nudipes* (Fuckel) Sacc. var. *nudipes* and *D. nudipes* var. *minor* Dennis [both now treated

as synonyms of *L. nudipes*], but our ascomata and ascospore measurements are closer to his *D. nudipes* var. *minor*.

Lachnum nudipes has been reported on *Epilobium, Filipendula,* and *Spiraea* in Europe (Dennis 1949, as *Dasyscypha*). This is the first record *Lachnum nudipes* for Mexico and the first report of its occurrence on ferns.

Lachnum pteridophyllum (Rodway) Spooner,
Biblioth. Mycol. 116: 470 (1987). FIGS 27, 28

Macro and micromorphological characters agree with the description of Medel & Lorea-Hernández (2008).

HABITAT—On rachises of *Cyathea divergens* var. *tuerckheimii, Cyathea* sp., *Dryopteris* sp., and *Lophosoria quadripinnata.*

SPECIMENS EXAMINED—**MEXICO. VERACRUZ, San Andrés Tlalnelhuayocan County**, El Riachuelo, 13 October 2011, Baeza 29, 52, 53; 4 November 2011, Baeza 60, Medel 2196; 8 December 2011, Medel & Lorea 2214. Los Encinales, 19°31.10′N 97°00.32′W, 1630 m, 10 August 2011, Baeza 36. 19 August 2011, Medel 2179, 2182, 2185.

Lachnum pteridophyllum has been reported from Colombia, Dominican Republic, Jamaica, Mexico, Panama, Peru, Puerto Rico, New Guinea, New Zealand, Taiwan, Tasmania, and Venezuela (Haines 1980, Medel & Lorea-Hernández 2008). Haines (1980) cited this species on *Cyathea sp.* from Oaxaca (Mexico), and Medel & Lorea-Hernández (2008) from Veracruz on decaying leaves of *Dicksonia sellowiana, Cyathea divergens* var. *tuerckheimii,* and *Cyathea* spp. We add now two more hosts: *Dryopteris* sp. and *Lophosoria quadripinnata.*

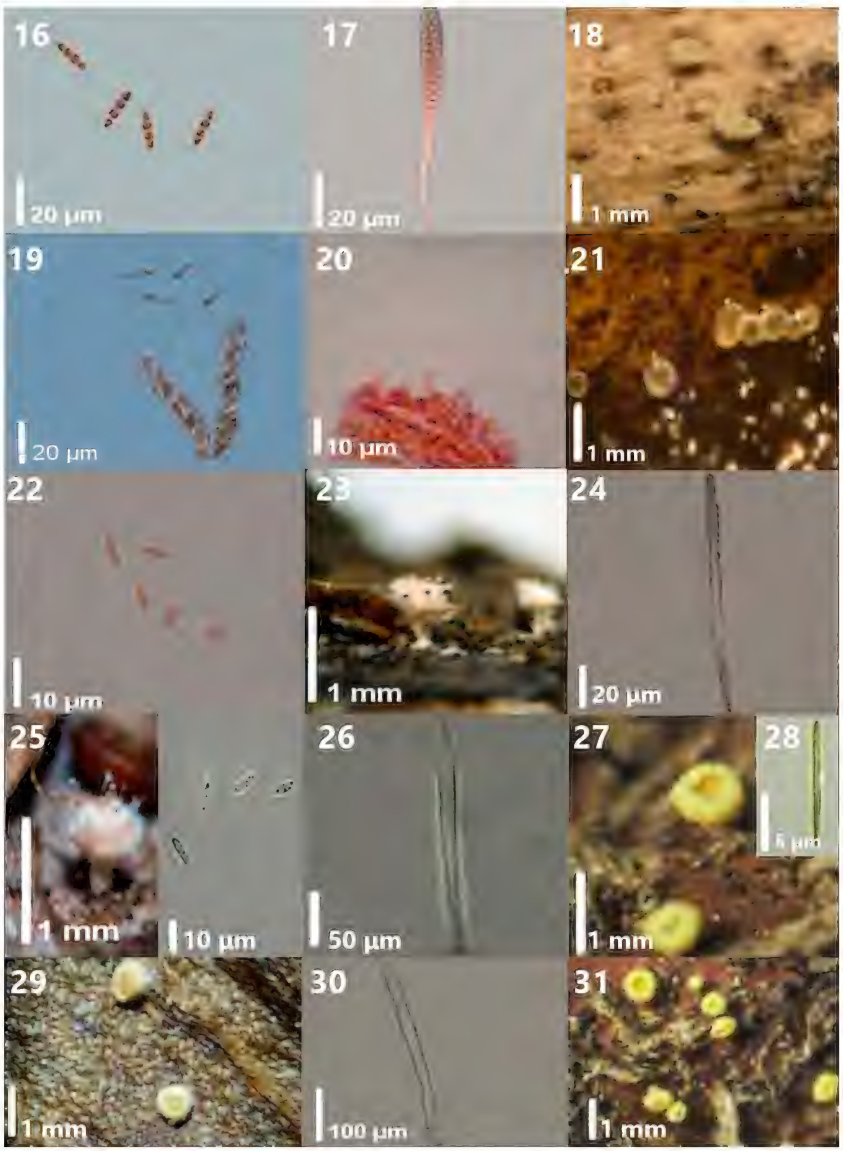
Lachnum singerianum (Dennis) W.Y. Zhuang & Zheng Wang,
Mycotaxon 67: 27 (1998). FIGS 29, 30

Macro and micromorphological characters agree with the description of Medel & Lorea-Hernández (2008).

HABITAT—On rachises of *Alsophila firma* and *Dicksonia sellowiana.*

SPECIMEN EXAMINED—**MEXICO. VERACRUZ: San Andrés Tlalnelhuayocan County**, Río Xocoyolapan, 19°30.89′N 97°00.39′W, 1590 m; 8 December 2011, Medel 2222.

Lachnum singerianum is known from the Andean region in South America from Bolivia to Venezuela and from China, Jamaica, and Mexico (Haines 1980, Medel & Lorea-Hernández 2008). Haines (1980) earlier reported *L. singerianum* growing on rachises of ferns, while Medel & Lorea-Hernández (2008) reported the species on decaying leaves of *Alsophila firma* and *Dicksonia sellowiana* in Veracruz.



Figs 16–31. ***Durella macrospora.*** 16. Three-septate ascospores; 17. Asci with 1-septate ascospores. ***Hamatocanthoscypha helicotricha.*** 18. Apothecia; 19. Asci and ascospores; 20. Uncinate or coiled hairs. ***Hyaloscypha fuckelii.*** 21. Apothecia; 22. Ascospores. ***Lachnum brevipilosum.*** 23. Apothecium; 24. Septate hairs. ***Lachnum nudipes.*** 25. Apothecium (left) and ascospores (right); 26. Lanceolate paraphysis. ***Lachnum pteridophyllum.*** 27. Apothecium; 28. Ascospores. ***Lachnum singerianum.*** 29. Apothecium; 30. Septate hair in 5% KOH. ***Lachnum varians.*** 31. Apothecia.

Lachnum varians (Rehm) M.P. Sharma,
Nova Hedwigia 43: 411 (1986). FIGS 31, 32

Macro and micromorphological characters agree with the description of Medel & Lorea-Hernández (2008).

HABITAT—On rachises of *Cyathea bicrenata* and *C. divergens* var. *tuerckheimii* and fronds of *Adiantum andicola.*

SPECIMENS EXAMINED—**MEXICO. VERACRUZ: San Andrés Tlalnelhuayocan County**, El Riachuelo, 19°30.99′N 97°00.39′W, 1626 m 18 August 2011, Baeza 47b, Córdova 68, 69; 8 December 2011, Baeza 70.

ADDITIONAL SPECIMENS EXAMINED: **MEXICO. VERACRUZ: Xalapa County,** Santuario del Bosque de Niebla, Parque Ecológico Francisco Javier Clavijero, 1 September 2013, Medel & Lorea 2259.

Lachnum varians is known from Australia, Hawaii, Mexico, New Guinea, New Zealand, South America, and the Caribbean (Haines 1980, Medel & Lorea-Hernández 2008). The species was previously reported only on decaying leaves of *Alsophila firma* (Medel & Lorea-Hernández 2008); the present study adds the new hosts *Cyathea bicrenata, C. divergens* var. *tuerckheimii,* and *Adiantum andicola.*

Lachnum virgineum (Batsch) P. Karst.,
Bidrag Kännedom Finlands Natur Folk 19: 169 (1871). FIGS 33, 34

APOTHECIA superficial, cupulate, 1–1.3 mm diam. Disc flat to concave, white to yellowish white (1A1-1A2). Receptacle densely covered with short, broad, white (1A1) hairs. Stipe, thin, covered with hairs concolorous with the apothecia. HAIRS cylindrical, 60 × 5–6(–8) µm, granulose along the entire length, 3–4-septate, the apex broadening ≤8 µm diam. ASCI cylindric-clavate, 42–51× 4–5 µm, 8-spored, biseriate, pore weakly blue (J+). ASCOSPORES fusiform, ends rounded, with one end sometimes wider than the other, (6–)7–8 × 1–2 µm (Q = 4.6). PARAPHYSES lanceolate 4–5 µm diam., 2–3-septate, with small refractive guttules in the apex, extending beyond the asci by 20 µm.

HABITAT—On fronds of *Phlebodium aureum.*

SPECIMENS EXAMINED—**MEXICO. VERACRUZ: San Andrés Tlalnelhuayocan County**, El Riachuelo, 10 August 2011, Baeza 32; 8 December 2011, Medel 2208.

The Mexican specimens fit well the description of *Lachnum virgineum* (Spooner 1987), especially the shape, color, and size of the apothecium (densely covered by white hairs), spore size, and paraphyses exceeding the asci by 15–20 µm. *Lachnum virgineum* is similar to *L. controversum* (Cooke) Rehm, which differs in obtuse or slightly swollen hair apexes and very slightly

narrower (3.5–4.5 µm diam.) paraphyses. Although *L. virgineum* is generally regarded as lignicolous, we found it growing on fronds of *Phlebodium aureum*. Known from Australia and Europe (Breitenbach & Kränzlin 1984, Spooner 1987).

Mollisia ventosa P. Karst.,
Bidrag Kännedom Finlands Natur Folk 19: 188 (1871). FIGS 35–37

APOTHECIA superficial, sessile, discoid, flat, 0.5–1 mm diam., greenish-yellow (1A7) with dark grey (1F1) to olive gray (1D2) margin. Receptacle greenish gray (29F2), smooth. ASCI (72–)85–115 × 7–8(–10) µm, apical pore J+. ASCOSPORES ellipsoid, (9–)12–15(–16) × 1.5–2 µm (Q = 7.5), 1–3-septate, guttulate. PARAPHYSES filiform, slender, septate, branched or not. ECTAL EXCIPULUM a textura angularis to textura globulosa, cells thick-walled, brownish, 6–10(–12) × 6–10 µm.

HABITAT—On rachises of *Cyathea bicrenata.*

SPECIMENS EXAMINED—**MEXICO. VERACRUZ: San Andrés Tlalnelhuayocan County**, El Riachuelo, 19°30.99′N 97°00.39′W, 1626 m, 4 November 2011, Medel 2196; 8 December 2011, Baeza 71, Baeza 72.

Mollisia ventosa has been reported from Europe, and America (Breitenbach & Kränzlin 1984, Dennis 1950, 1978, Medel & Chacón 1997). Dennis (1950, 1978) described *M. ventosa* with spores larger (10–20 × 2–3.5 µm) than those in our Mexican collections, which instead match the measurements cited by Breitenbach & Kränzlin (1984). They cited *M. ventosa* as growing on *Alnus* and decorticated wood, but not on ferns. *Mollisia undulatodepressula* (Feltgen) Le Gal & F. Mangenot, the only other *Mollisia* species known to inhabit cloud forests in Mexico, grows on rotten wood (Medel & Chacón 1997).

Orbilia auricolor (A. Bloxam) Sacc.,
Syll. Fung. 8: 625 (1889). FIGS 38, 39

APOTHECIA superficial, scattered, sessile, cup-shaped. DISC concave, 0.8–1 mm diam., yellow brownish to yellow gray (4B3-4B5) translucent when rehydrated, margin crenulate. RECEPTACLE concolorous with disc, smooth. ASCI cylindric-clavate, 30–40(–42) × 2–4 µm, hyaline, thin-walled, 8-spored, biseriate, pore J–, base forked. ASCOSPORES curved-filiform, (8–)9–10 × 1 µm (Q = 8.8), smooth, hyaline. PARAPHYSES cylindrical, apex capitate, with incrustations, 3–4 µm diam., septate, branched at base. ECTAL EXCIPULUM textura globulosa with hyaline cells.

Habitat—On rachises of *Cyathea bicrenata* and *Marattia laxa.*

Specimens examined—**MEXICO. Veracruz: San Andrés Tlalnelhuayocan County**, Río Xocoyolapan 19°30.89′N 97°00.39′W, 1590 m, 8 December 2011, Baeza 67, Medel 2202.

The morphology of the apothecia, ascospores, asci, and paraphyses in our Mexican specimens agree with *Orbilia auricolor* as described by Spooner (1987) and Mo & al. (2005). The asexual stage of *O. auricolor* has been recorded (as *Arthrobotrys oligospora* Fresen.*)* from Xochimilco, Mexico (Chavarria & al. 2010).

Orbilia auricolor is known from Asia, Australia, Europe (Breitenbach & Kränzlin 1984, Dennis 1981, GBIF 2019, Mo & al. 2005, Spooner 1987). The species has previously been recorded growing on dead wood and woody stems and other plant matter (Spooner 1987, Mo & al. 2005), but not on ferns.

Protocreopsis pertusa (Pat.) Samuels & Rossman, Stud. Mycol. 42: 66 (1999). Figs 40, 41

Perithecia aggregated, globose, sessile, 0.8–1 mm diam., covered by whitish (2A1) to yellowish white (3A2) hairs. Hairs cylindrical, curved to wavy, smooth, thick-walled, hyaline, apices simple or forked, septate. Subiculum of thin whitish (2A1) hyphae, attached to the perithecia. Asci clavate-cylindrical, 75–95(–100) × 10–12 µm, thin-walled, hyaline, ascospores irregularly biseriate, 8–spored, base with croziers. Ascospores ellipsoid, (13–)14–16 × 5 µm (Q = 2.7), smooth, hyaline, 1-septate, with two large guttules in the ends. Paraphyses filiform and hyaline.

Habitat—On rachises of *Alsophila firma* and *Marattia laxa.*

Specimens examined—**MEXICO. Veracruz: San Andrés Tlalnelhuayocan County**, Río Xocoyolapan, 19°30.89′N 97°00.39′W, 1590 m, 13 October 2011, Córdova 77; 8 December 2011, Baeza 68, Medel & Lorea 2205.

Additional specimens examined: **MEXICO. Veracruz: San Andrés Tlalnelhuayocan County,** Rancho Agüita Fria, 6 April 2007, Medel 1362.

Rossman & al. (1999) and Chaverri & al. (2010) described *Protocreopsis pertusa* as having thin white mycelium beneath each perithecium, thick-walled hairs densely united around the perithecial opening, and 1–3-septate spores measuring 13–17 × 4–5 µm, all characters agreeing with our Mexican specimens. This species has been reported from tropical to subtropical regions on leaves of *Musa*, *Heliconia*, palms, bamboos, and fern rachises. It is a new record for Mexico.

Figs 32–48. ***Lachnum varians.*** 32. Asci with ascospores. ***Lachnum virgineum.*** 33. Apothecia; 34. Hair with enlarged apex. ***Mollisia ventosa.*** 35. Apothecia; 36. Excipulum at margin and lower flank; 37. Asci with ascospores. ***Orbilia auricolor.*** 38. Apothecia 39. Paraphysis. ***Protocreopsis pertusa.*** 40. Apothecia 41. Ascospores. ***Seimatosporium tostum.*** 42. Stromata 43. Asci with ascospores, 44. Ascospores. ***Stictis carnea.*** 45. Apothecia. 46. Ascospores. ***Stictis radiata.*** 47. Apothecia; 48. Asci and ascospores.

Seimatosporium tostum (Berk. & Broome) Rossman & W.C. Allen, IMA Fungus 7(1): 5 (2016). Figs 42–44

Stromata shield-like, growing within host tissue, black, grey (30F1) to greenish grey (30F2) pigments are observed in KOH. Two perithecia per stroma. Asci cylindrical, 62–75 × 5–7(–8) µm, thin-walled, apical pore J+, spores 1–2-seriate, without croziers. Ascospores ellipsoidal-fusiform, 1-septate, constricted at the septum, smooth, poles subacute to acute, (9–)10–11(–12) × 3–4 µm (Q = 2.3). Paraphyses filiform, ≤1 µm diam., extending beyond the ascus by 3–5 µm, with tiny hyaline guttules at the apex.

Habitat—On rachises of *Alsophila firma* and *Cyathea bicrenata.*

Specimens examined—**MEXICO. Veracruz: San Andrés Tlalnelhuayocan County**, Río Xocoyolapan, 19°30.89′N 97°00.39′W, 1590 m, 8 December 2011, Medel & Lorea 2108; 26 February 2001, Medel & Lorea 2201; Los Encinales, 19°31.10′N 97°00.32′W, 1630 m, 30 March 2014, Medel & Lorea 2379.

Additional specimens examined: **MEXICO. Veracruz: San Andrés Tlalnelhuayocan,** Rancho Agüita Fría, 7 February 2007, Medel 1342.

Seimatosporium tostum is described by Paulus & al. (2006) as having larger (>14 × 5 µm) hyaline ascospores with only one septum, while Brockmann (1976) described North American material (as *Discostroma tostum*) with 1–6-septate ascospores. The species has been reported growing on stems of *Epilobium*. Known from North America (Brockmann 1976, Paulus & al. 2006), *S. tostum* establishes a new record for Mexico and the first report on ferns.

Stictis carnea Seaver & Waterston, Mycologia 33: 311 (1941). Figs 45, 46

Apothecia immersed in host tissue, hymenium greyish yellow to light yellow (1A5-1B6), 05–0.7 mm diam., surrounded by an elliptical white (1A1) ring. Asci cylindric-clavate, 110–150 × 6–7 µm, 8-spored, hyaline, J–. Ascospores long filiform, (80–)85–130(–150) × 3 µm, tapering to one end, multi-septate, twisted within the ascus. Paraphyses filiform, ≤3 µm wide, longer, hyaline, septate.

Habitat—On rachises of *Cyathea bicrenata.*

Specimen examined—**MEXICO. Veracruz: San Andrés Tlalnelhuayocan County**; Río Xocoyolapan; 19°30.89′N 97°00.39′W, 1590 m, 4 November 2011, Medel 2112.

There are two species of *Stictis* growing on ferns in our study site, *S. carnea* and *S. radiata.* The differences in spore length and apothecial morphology of the apothecia are sufficient to separate these two species (Sherwood 1977,

Johnston 1983). *Stictis carnea* has been reported from Asia, North America (including Mexico), and New Zealand (Johnston 1983, Sherwood 1977), growing on dead tissues of many herbaceous and woody plants and the fern *Cyathea medullaris* (Johnston 1983). This species is a new report from Mexico.

Stictis radiata (L.) Pers., Observ. Mycol. 2: 73 (1800 ["1799"]). FIGS 47, 48

APOTHECIA deeply sunken in host tissue, hymenium vivid yellow to yellow (3A7-3A8), ≤1 mm diam., surrounded by an irregular white (1A1) ring. ASCI cylindric-clavate, 240–290 × (7–)10–12 µm, 8-spored, hyaline, narrowed toward the apex, pore J–. ASCOSPORES long filiform, (219–)245–280(–283) × 2–3 µm, multiseptate, spirally arranged within the ascus. PARAPHYSES filiform, 1 µm diam., slightly widening (≤2 µm) at the apex.

HABITAT—On rachises of *Alsophila firma, Cyathea bicrenata, Sphaeropteris horrida,* and fronds of *Polypodium* sp.

SPECIMENS EXAMINED—**MEXICO. VERACRUZ: San Andrés Tlalnelhuayocan County**; Río Xocoyolapan; 19°30.89′N 97°00.39′W, 1590 m, 4 November 2011, Medel 2199; 8 December 2011, Baeza 69, Medel & Lorea 2200. Paraje El Riachuelo, 8 December 2011; Medel & Lorea 2207. Los Encinales, 19°31.10′N 97°00.32′W, 1630 m, 10 August 2011, Baeza 38b, Medel & Lorea 2169.

Diagnostic characters of *Stictis radiata* include ascomata with a deeply sunken orange yellow hymenium and filiform multiseptate spores with interlaced arrangement within the ascus and variably sized (180–325 × 1.9–2.8(–3) µm; Breitenbach & Kränzlin 1984, Johnston 1983, Sherwood 1977). *Stictis radiata* resembles *S. carnea* but is distinguished by its shorter and wider ascospores. Known from Mexico, New Zealand, and Australia (Johnston 1983, Sherwood 1977). In New Zealand, *S. radiata* has been reported on the ferns *Cyathea dealbata* and *Dicksonia squarrosa* (Johnston 1983). We found *S. radiata* also growing on *Sphaeropteris horrida* and *Polypodium* sp.

Discussion

Ferns, which comprise many genera and families, serve as habitat for a large number of fungi. Our study indicates that most of the fungi on ferns belong to *Lachnaceae* [previously included in *Hyaloscyphaceae* s.l.], represented by eight species of *Lachnum*. Haines (1980), Samuels & Rogerson (1980), and Medel & Lorea-Hernández (2008) previously reported *Hyaloscyphaceae* s.l. on ferns. Medel (2013), who conducted earlier research on Mexican cloud forest ascomycetes, pointed out that *Lachnaceae* is "recurrent" on ferns in *Cyatheaceae,* indicating that some of these fungi may live as endophytes in this fern family.

The dominant plant associates in this study belong to the "tree ferns"—*Alsophila firma, Cyathea bicrenata*, *C. divergens* var. *tuerckheimii*, and *Sphaeropteris horrida*. Herbaceous fern species with short stems at or barely above ground level include *Dryopteris* sp., *Lophosoria quadripinnata*, *Marattia laxa*, and *Thelypteris* spp. *Adiantum andicola* and *Sticherus palmatus* are classed as herbs with underground stems, while *Grammitis* sp., *Phlebodium aureum, Pecluma alfredii*, and *Polypodium* sp., represent a diverse epiphytic fern group. Two fern species hosted the highest number of fungal species: *Alsophila firma* (11 species) and *Cyathea bicrenata* (12 species). The ascomycetes identified in this study grew more frequently on petioles and rachises of tree ferns and some herbaceous ferns.

Our work stresses the importance of studying the highly diverse small ascomycetes given that new records have been established by every study (Braun 2004, Braun & al. 2013, Cannon 1997, Castañeda-Ruiz & Heredia 2000, Del Olmo & Arnolds 2014, Dingley 1972, Haines 1980, Kirschner & Liu 2014, Medel & Lorea-Hernández 2008, Samuels & Rogerson 1990, Stevenson 1945); unfortunately, few have studied species from the Western Hemisphere. This paper contributes new fern families and genera to the list of ascomycetes hosts: *Dicksoniaceae* (genus *Lophosoria*), *Marattiaceae* (*Marattia*), and *Polypodiaceae* (*Grammitis* and *Pecluma)*. This is important since there are few studies on the diversity of fungi on ferns, and most have dealt only with genera of tree ferns in *Cyatheaceae* and *Dicksoniaceae.*

According to the literature surveyed, only seven ascomycete species had previously been registered on ferns from Veracruz. This study adds 18 more records associated with ferns in Mexican cloud forests, bringing the

Table 1. Ascomycete fungi and fern hosts recorded from Mexico

Species	Host	Reference
Helotiales		
Arachnopezizaceae		
cf. *Arachnopeziza*	*Alsophila firma*	This paper
Dermataceae		
*Mollisia ventosa**	*Cyathea bicrenata*	This paper
Helotiaceae		
*Bisporella pteridicola**	*Alsophila firma, Cyathea bicrenata, Pecluma alfredii, Sphaeropteris horrida, Thelypteris* sp.	This paper
*Crocicreas quinqueseptatum**	*Cyathea bicrenata*	This paper

Crocicreas sessilis	*Cyathea divergens* var. *tuerckheimii*	Samuels & Rogerson 1990
Cyathicula sp.	*Cyathea bicrenata*	This paper
*Durella macrospora**	*Sticherus palmatus*	This paper
Hyaloscyphaceae		
*Dasyscyphella dryina**	*Alsophila firma*	This paper
*Hamatocanthoscypha helicotricha**	*Cyathea bicrenata, Sticherus palmatus*	This paper
*Hyaloscypha fuckelii**	*Alsophila firma*	This paper
Lachnaceae		
*Lachnum brevipilosum**	*Alsophila firma, Cyathea bicrenata*	This paper
Lachnum fimbriiferum	*Alsophila firma, Cyathea bicrenata, Cyatheaceae, Dicksonia sellowiana*	Medel & Lorea-Hernández 2008
Lachnum nudipes *	*Lophosoria quadripinnata*	This paper
Lachnum oncospermatum	*Dicksonia sellowiana*	Medel & Lorea-Hernández 2008
Lachnum pteridophyllum	*Cyathea divergens var. tuerckheimii, Cyathea* sp., *Dicksonia sellowiana,* ***Dryopteris* sp.**, ***Lophosoria quadripinnata***	Haines 1980; Medel & Lorea-Hernández 2008
Lachnum singerianum	*Alsophila firma, Dicksonia sellowiana*	Medel & Lorea-Hernández 2008
Lachnum varians	*Alsophila firma,* ***Cyathea bicrenata, C. divergens* var. *tuerckheimii, Adiantum andicola***	Haines 1980; Medel & Lorea-Hernández 2008
Lachnum virgineum	*Phlebodium aureum*	This paper
Paradiopsidaceae		
Dimeriella polypodii	*Polypodium montigenum, P. madrense*	Samuels & Rogerson 1990
Hypocreales (*Bionectriaceae*)		
*Protocreopsis pertusa**	*Alsophila firma, Marattia laxa*	This paper
Orbiliales (*Orbiliaceae*)		
*Orbilia auricolor**	*Cyathea bicrenata, Marattia laxa*	This paper
Ostropales		
Coenogoniaceae		
Coenogonium botryosum	*Adiantum andicola, Grammitis* sp.	This paper
Stictidaceae		
*Stictis carnea**	*Cyathea bicrenata*	This paper
*Stictis radiata**	*Alsophila firma, Cyathea bicrenata,* ***Sphaeropteris horrida, Polypodium* sp.**	This paper
Xylariales (*Sporocadaceae*)		
Seimatosporium tostum	*Alsophila firma, Cyathea bicrenata.*	This paper

Bold face indicates new hosts for the corresponding fungus

* indicates new fungal records for Mexico

total to 25 ascomycete species distributed among *Helotiales* (20 species), *Hypocreales* (1), *Ostropales* (3), and *Xylariales* (1). Taxonomic diversity of *Ascomycota* reported in similar studies from other regions of the world show a wide diversity of ascomycetes involved in biological interaction with ferns. For example, Del Olmo & Arnolds (2014) reported the primary endophytes to inhabit ferns in Costa Rica belonged to *Dothideomycetes*, *Eurotiomycetes,* and *Sordariomycetes,* while mycosphaerellaceous fungi were more abundant in Taiwan (Kirschner & Liu 2014) and other countries in Asia and Africa (Braun & al. 2013). Only Haines (1980) cited *Helotiales* (*Hyaloscyphaceae* s.l.) as the predominant fungi on tropical ferns, further supported by this study where *Lachnaceae* was the most diverse family represented. To find such diversity of ascomycetes associated with ferns, almost quadrupling the number of species previously known for Mexico, suggests there are several taxa yet to discover. We agree with Kirschner & Liu (2014) that research on ascomycetes growing on ferns is still in its infancy. Additional work is needed to establish the ecology of fern-associated fungi, particularly the recurrence of some taxa on fern hosts.

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First sexual morph record of *Sarcopodium vanillae*

Napalai Chaiwan[1,2], Sajeewa S.N. Maharachchikumbura[3], Dhanushka N. Wanasinghe[2], Mingkwan Doilom[2], Ruvishika Jayawardena[1], Kevin D. Hyde[1,2*]

[1] *Center of Excellence in Fungal Research, Mae Fah Luang University, Chiang Rai 57100, Thailand*

[2] *Key Laboratory for Plant Diversity and Biogeography of East Asia, Kunming Institute of Botany, Chinese Academy of Science, Kunming 650201, Yunnan, People's Republic of China*

[3] *School of Life Science and Technology, University of Electronic Science and Technology of China, Chengdu 611731, People's Republic of China*

* Correspondence to: *kdhyde3@gmail.com*

Abstract—*Sarcopodium vanillae* was isolated from a dead leaf of *Dracaena* in Chiang Rai Province, Thailand. Combined analyses of ACT, ITS, LSU, and tub2 sequence data obtained from the cultures derived from single spore isolates confirm that our collections represent *S. vanillae*. This is the first record of the sexual morph, and the first record of *S. vanillae* from *Dracaena*. A description and illustrations of both sexual and asexual stages of *S. vanillae* are provided.

Key words—multigene, new host record, *Nectriaceae*, saprobe, taxonomy

Introduction

During our research on the diversity of microfungi in Thailand, we recovered isolates from *Dracaena* in Chiang Rai Province that were typical of *Nectriaceae* based on our preliminary morphological studies. Further morphological and molecular characterization (multigene-based phylogeny of nuclear ribosomal and protein-coding loci ACT, ITS, LSU and Tub2 sequence data) revealed the taxon as *Sarcopodium vanillae*. *Nectriaceae* (*Hypocreales;* Rossman & al. 1999, Maharachchikumbura & al. 2015) is typified by a characteristic perithecial wall structure and specific anamorphic

states. Its uniloculate perithecioid ascomata are yellow, orange, red, purple or white, and the asexual morph is phialidic (Rogerson 1970, Rehner & Samuels 1995). The genus *Sarcopodium* Ehrenb. has had numerous nomenclatural changes since it was first described in 1818 that have been synonymised under *Sarcopodium*.

Cyphina Sacc., had already been synonymised under *Sarcopodium* by Sutton (1977) and under "one fungus: one name" by Rossman & al. (2016) supported the placement of the (asexual) *Actinostilbe* and the (sexual) *Lanatonectria* under the much earlier (asexual) *Sarcopodium*. *Sarcopodium* Ehrenb. is closely related to *Pseudonectria* Seaver. (Rossman & al. 1999). Sutton (1981) synonymized *Actinostilbe* Petch. under *Sarcopodium*; and all five species of *Lanatonectria* Samuels & Rossman (a genus described from a sexual morph) have been transferred to *Sarcopodium* following phylogenetic analyses (Lombard & al. 2015, Pennycook & Kirk 2019a). The new epithet for the type species (*"flocculentum"*) has priority over the previous heterotypic synonym, *Sarcopodium macalpinei* (Pennycook & Kirk 2019b).

Some *Sarcopodium* species have both sexual and asexual morphs, but *S. vanillae* has been known only from its asexual morph (Sutton 1981; Rossman 1983, 1996, 2000; Rossman & al. 1993, 2013, 2016). This paper describes the first record of a sexual morph for *S. vanillae* and reports *Dracaena* as a new host record for this fungus.

Materials & methods

Sample collection, morphological study and isolation

Dead leaves of *Dracaena* were collected from Chiang Rai Province in Thailand during November 2017. The samples were taken to the laboratory in Zip-lock bags. Micro-morphological structures were observed and photographed with a Canon EOS 600D digital camera fitted to a Nikon Eclipse Ni compound microscope. Single spore isolates were obtained using the method described in Chomnunti & al. (2014). Germinated spores were transferred to potato dextrose agar (PDA) plates and incubated at 25–30 °C. Growth rates and culture characteristics were recorded after three weeks. The morphological characters were measured using Tarosoft (R) Image Frame Work v. 0.9.7 software. Figures were processed with an Adobe Photoshop CS6 Extended v. 10.0 software. The cultures are deposited in Mae Fah Luang University Culture Collection, Chang Rai, Thailand (MFLUCC). Specimens are deposited in the herbarium of Mae Fah Luang University, Chang Rai, Thailand (MFLU).

DNA extraction, PCR amplification and sequencing

Fungal isolates were grown on PDA for 3–4 weeks at 30 °C. The genomic DNA was extracted from mycelium using the E.Z.N.A. Forensic DNA Kit. Amplification

Table 1. Sequences from *Pseudonectria* and *Sarcopodium* species (and *Stachybotrys chartarum* outgroup) used in the phylogenetic analysis

Taxon	Culture no.	GenBank accession no.			
		ACT	ITS	LSU	tub2
P. buxi	CBS 324.53	KM231171	KM231778	KM231644	KM232037
P. foliicola	CBS 122566	KM231170	KM231777	KM231643	KM232036
S. circinatum	CBS 587.92	KM231180	KM231787	KM231651	KM232046
	CBS 100998	KM231179	KM231786	KM231650	KM232045
S. circinosetiferum	CBS 100251	KM231175	KM231782	KM231646	KM232041
S. flavolanatum	CBS 112283	KM231178	KM231785	KM231649	KM232044
	CBS 128370	KM231177	KM231784	KM231648	KM232043
S. macalpinei	CBS 115296	KM231176	KM231783	KM231647	KM232042
S. vanillae	CBS 100582	KM231173	KM231780	HQ232174	KM232039
	MFLU 17-2595	**MK692541**	**MK608516**	**MK691503**	**MK962543**
	MFLU 17-2597	**MK692542**	**MK685870**	**MK691502**	**MK692544**
Stachybotrys chartarum	CBS 129.13	KM231268	KM231858	KM231738	KM232127

New sequences are set in **bold** font.

primers used were: internal transcribed spacer (ITS)—ITS5 and ITS4 (White & al. 1990); 28S large subunit ribosomal RNA (LSU)—LROR and LR5 (Rehner & Samuels 1994, Vilgalys & Hester 1990); partial actin gene (ACT)—ACT-512F and ACT-783R (Carbone & Kohn 1999); partial beta-tubulin gene (tub2)—Bt-2a and Bt-2b (Glass & Donaldson 1995). The PCR mixer comprised 1 µl forward primer, 1 µl reverse primer, 9.5 µl distilled deionized (DD) water, and 12.5 µl mixer. The PCR conditions for ITS and LSU were 3 min at 94 °C; followed by 35 cycles of 30 s at 94 °C, 50 s at 55 °C, and 90 s at 72 °C; and a final elongation step at 72 °C for 10 min. Conditions for ACT were an initial elongation step of 2 min at 95 °C; followed by 35 cycles of 45 s at 95 °C, 45 s at 55 °C, and 1 min at 72 °C; and a final elongation step of 10 min at 72 °C. Conditions for tub2 were an initial 8 min of 95 °C; followed by 35 cycles of 30 s at 95 °C, 30 s at 55 °C, and 1 min at 72 °C; and a final elongation step at 72 °C for 5 min. The PCR products were purified and sequenced at Shanghai Sangon Biological Engineering Technology and Service Co. Isolates including accession numbers of gene sequences are listed in Table 1.

Phylogenetic analysis

Sequence data of *Sarcopodium vanillae* and related taxa (Table 1) were downloaded from GenBank following Zeng & al. (2018) and Yang & al. (2018). The multiple sequence alignments were produced with MAFFT v. 7 (http://mafft.cbrc.jp/

alignment/server/index.html) and BioEdit v. 7.0.5.2 (Hall 1999). The phylogenetic analyses were performed using maximum likelihood (ML) trees and generated using the RAxML-HPC2 on XSEDE (8.2.8) (Stamatakis & al. 2008, Stamatakis 2014) in the CIPRES Science Gateway platform (Miller & al. 2010) using GTR+I+G model of evolution. Parsimony analysis was carried out with the heuristic search option in PAUP v. 4.0b10 (Swofford 2002) using the following parameters: characters unordered with equal weight, random taxon addition, branch swapping with tree bisection-reconnection (TBR) algorithm, branches collapsing if the maximum branch length was zero. Alignment gaps were treated as missing characters in the combined data set, where they occurred in relatively conserved regions. Trees were inferred using the heuristic search option with 1000 random sequence additions, with maxtrees set at 1000. Descriptive tree statistics for parsimony; tree length (TL), consistency index (CI), retention index (RI), relative consistency index (RC) and homoplasy index (HI) were calculated for trees generated. The Kishino-Hasegawa tests (Kishino & Hasegawa 1989) were performed to determine whether trees were significantly different. Bayesian analysis was conducted with MrBayes v. 3.1.2 (Huelsenbeck & Ronquist 2001) to evaluate posterior probability (PP) (Rannala & Yang 1996) by Markov chain Monte Carlo sampling. GTR+I+G was used in the command. Six simultaneous Markov chains were run for 2,000,000 generations with trees sampled every 200th generation. The distribution of log-likelihood scores was examined to determine stationary phase for each search and to decide if extra runs were required to achieve convergence, using the program Tracer 1.4 (Rambaut & Drummond 2007). First 10% of generated trees were discarded and remaining 90% of trees were used to calculate posterior probabilities of the majority rule consensus tree. The phylogenetic tree was figured in FigTree v. 1.4 (Rambaut 2014) and edited using Microsoft Office Power Point 2007. Sequences derived in this study were deposited in GenBank (Table 1).

Phylogenetic results

The combined sequence alignments comprised 12 isolates, with *Stachybotrys chartarum* (CBS 129.13) as the outgroup taxon. The combined dataset comprised 3065 characters including alignment gaps, of which 844 were derived from ITS, 624 from LSU, 812 from ACT, and 785 from tub2. The MP analysis for the combined dataset had 415 parsimony informative, 2400 constant, 250 parsimony uninformative characters and yielded a single most parsimonious tree (TL = 1109, CI = 0.812, RI = 0.761, HI = 0.188, RC=0.617; Fig 1). The RAxML analysis of the combined dataset yielded a best scoring tree (Fig. 1) with a final ML optimization likelihood value of –9266.358949. The matrix had 656 distinct alignment patterns, with 17.28% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.220970, C = 0.279441, G = 0.267083, T = 0.232506; substitution rates

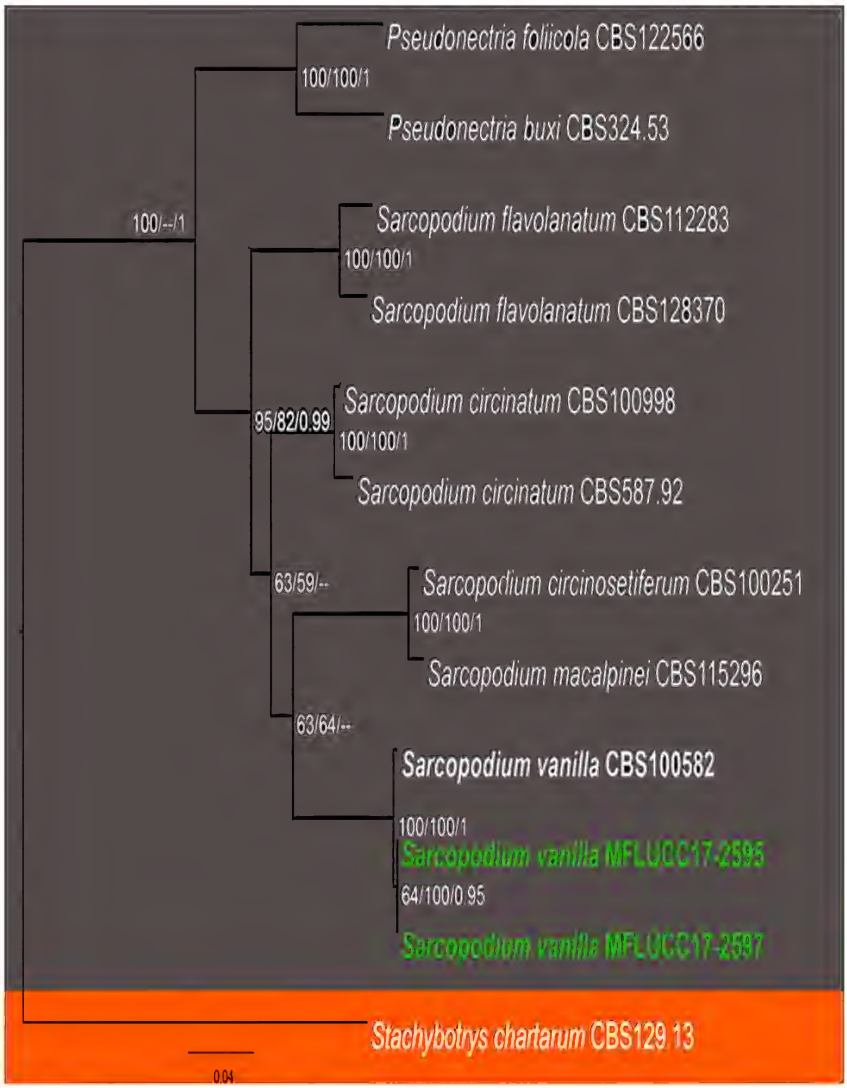

Fig. 1. Phylogram generated from RAxML based on combined ITS, LSU, ACT, and Tub2 sequence data. Bootstrap support values for maximum likelihood (ML) ≥60%, maximum parsimony (MP) ≥60%, and Bayesian posterior probabilities (PP) ≥0.95 are indicated as ML/MP/PP at the nodes. Ex-type strains are in bold and the strains from this study are indicated in green.

AC = 0.730175, AG = 1.879094, AT = 1.313827, CG = 0.798328, CT = 4.086170, GT = 1.000000; gamma distribution shape parameter α = 0.147281.

Bayesian posterior probabilities from Bayesian inference analysis were assessed with a final average standard deviation of split frequencies = 0.0056. The phylogenetic tree in this study showed that our strains (*Sarcopodium vanillae* MFLUCC 17-2595 and MFLUCC 17-2597) grouped in the *Sarcopodium* clade, and formed a well-supported cluster with *S. vanillae* (CBS 100582) with 64% ML, 100% MP, and 0.95 PP.

Taxonomy

Sarcopodium vanillae (Petch) B. Sutton,
Trans. Brit. Mycol. Soc. 76: 99 (1981) PLATES 1, 2
≡ *Actinostilbe vanillae* Petch, Ann. Roy. Bot. Gard. (Peradeniya) 9(3):327 (1925)

SAPROBIC on dead leaves of *Dracaena* (*Asparagaceae*).

SEXUAL MORPH: ASCOMATA 150–200 μm high, 160–240 μm wide (x = 173 × 189 μm, n = 5), perithecial, subglobose, solitary or in groups, soft-textured, pale yellow or rarely orange, superficial on a leaf or erumpent, with a papillate ostiole. PERIDIUM 15–25 μm wide (x = 47 μm, n = 5), composed of several layers of white to light orange cells of textura angularis. ASCI 36–52 × 3–5 μm (x = 44 × 4.5 μm, n = 20), 4-spored, unitunicate, cylindrical, rounded at apex, clavate to fusiform, short pedicellate. ASCOSPORES 8–12 × 3–4.5 μm (x = 11 × 3.9 μm, n = 20), fasciculate, broadly elongate, 1-septate.

ASEXUAL MORPH: MYCELIUM, branched, septate, hyaline, smooth. CONIDIOMATA 200–210 × 220–240 μm (x = 205 × 230 μm, n = 5), sporodochial, solitary or gregarious, setiferous, yellow to bright yellow or rarely orangish brown, soft-textured, superficial, separate, gregarious or confluent, sessile, attached to the substratum by a small stroma concentrated in the epidermis or outer layers of peridermal tissue, pulvinate, setose. SETAE 100–110 × 5–10 μm (x = 105 × 7.5 μm, n = 5), septate, unbranched, cylindrical, incurved, erect, very thick-walled, medium to pale golden brown, more or less straight (occasionally slightly bent either at the base or nearer the apex), erect, hyaline, pointed or rounded at the apex. CONIDIOPHORES mononematous, verticillately or penicillately branched, straight or flexuous, smooth, hyaline, short, septate, with 1–4 monochasial branching, compactly arranged, cylindrical, intermixed with long setae. CONIDIOGENOUS cells enteroblastic, monophialidic, integrated, cylindrical or more frequently tapered towards the apices, subulate, widest from middle to base, 10–20 × 1.2–2.7 μm (x = 15 × 1.95 μm, n = 5), with inconspicuous collarette, hyaline, smooth,

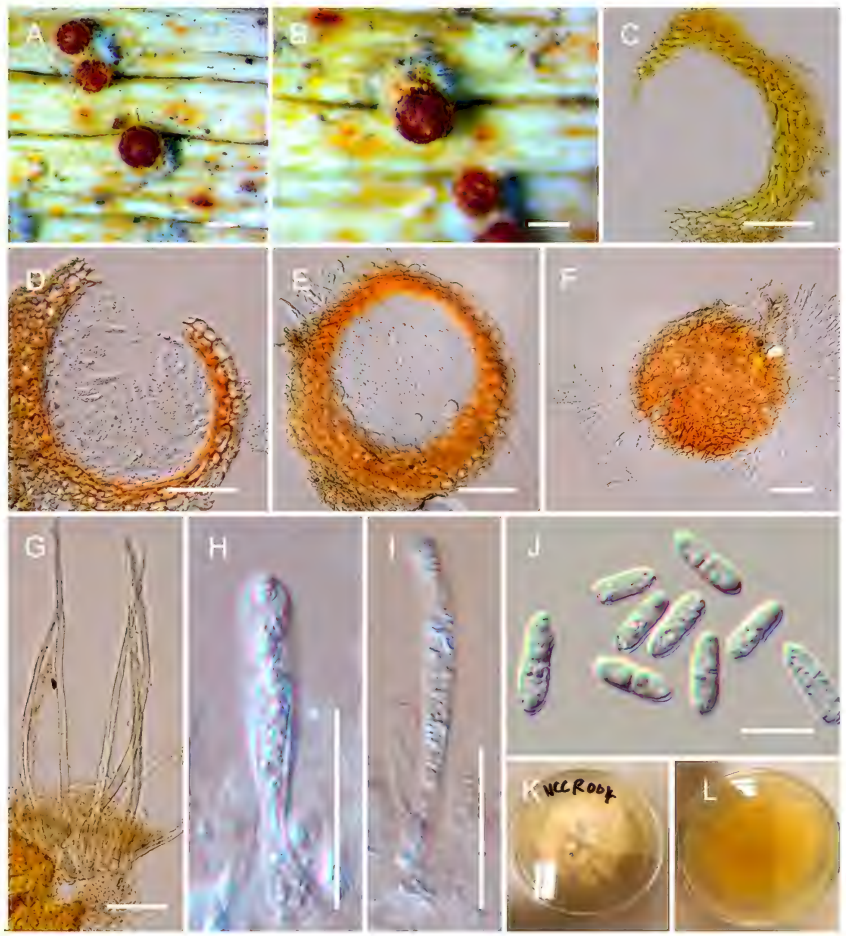

Plate 1. *Sarcopodium vanillae* (MFLU 19-0567, herbarium specimen): A, B. Perithecia on host surface; C–E. Perithecial cross sections; F. Crush mount of perithecium; G. Conidioma on perithecium; H, I. Asci, J. Ascospores; K, L. PDA cultures. Scale bars: A, B = 200 µm; C–G = 50 µm; H, I = 20 µm; J = 10 µm

formed as the ultimate branches of conidiophores and completely covering the external face of the conidiomata. Conidia 5–9 × 2.1–2.6 µm (x = 6 × 2.5 µm, n = 20), cylindrical, 0–1-septate, smooth, hyaline, rounded at both ends, held together in a slimy mass, ellipsoid to oval, straight.

Culture Characteristics: Colony on PDA reaching 30–40 mm diam. after 3 weeks at 25–30 °C; from above, white to yellow at margin, white to

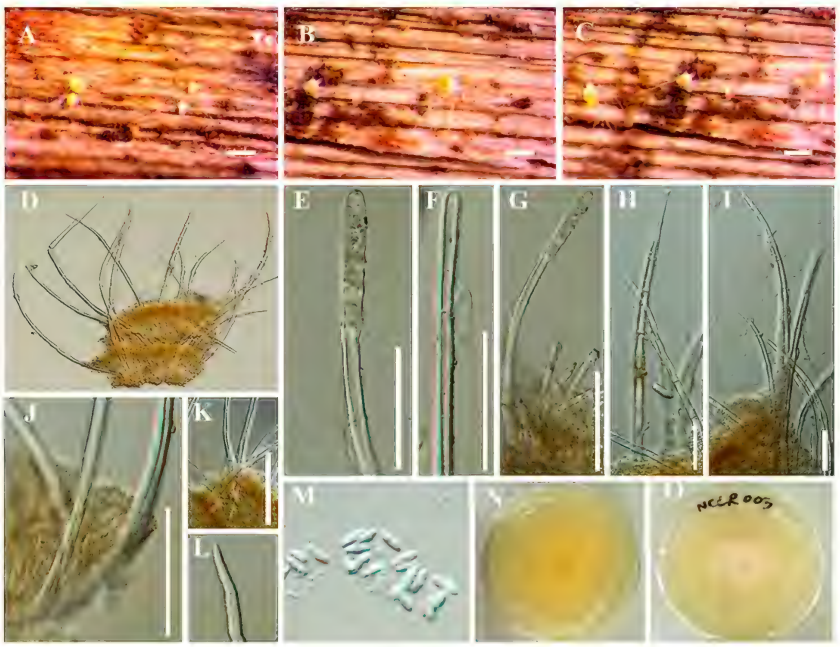

Plate 2. *Sarcopodium vanillae* (MFLU 19-0566, herbarium specimen): A–C. Conidiomata on host surface; D. Conidioma; E–I. Setae; J, K. Setal bases; L. Setal apex; M. Conidia; N, O. PDA cultures. Scale bars: A–C = 200 µm; D, J, K = 100 µm; E–I, L, M = 50 µm.

orange in the middle, white at centre; from below, yellow, medium dense, irregular, slightly raised to umbonate, surface slightly rough, dull with umbonate edge, concave at centre, fluffy to floccose, with white tufts at centre.

Specimens examined: **THAILAND**, **Chiang Rai Province**, **Mae Lao District**, on dead leaf of *Dracaena*, 17 November 2017, Napalai Chaiwan NCCR003 (MFLU 19-0566 [asexual morph]; living culture MFLUCC 17-2595); Napalai Chaiwan NCCR004 (MFLU 19-0567 [sexual + asexual morph]; living culture MFLUCC 17-2597).

Discussion

Our strains share similar morphological characters with *S. vanillae* strain CBS 100852, which was isolated from *Anthurium* sp. in Ecuador (Lombard & al. 2015). The phylogenetic analysis also supports the close relationship. The genus *Sarcopodium* has both sexual and asexual morphs (Wijayawardene & al. 2017a,b, 2018). The conidial morphology of our strain is similar to *S. circinatum* (the type species of the genus); however our conidiomata and conidiophores more closely resemble *Volutella ciliata* (CBS 483.61)

(Lombard & al. 2015). Previously, only the asexual morph has been observed for *S. vanillae* (Sutton 1981), and this study is the first report of the sexual morph. *Sarcopodium vanillae* has been reported from *Abelmoschus manihot* in Papua New Guinea, *Citrus nobilis* in Brunei, *Vanilla planifolia* in Sri Lanka, and *V. tahitensis* in Papua New Guinea (Farr & Rossman 2019). This study provides the first report of *S. vanillae* from *Dracaena*, and its first report from Thailand.

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Notes on rust fungi in China 7. *Aecidium caulophylli* life cycle inferred from phylogenetic evidence and renamed as *Puccinia caulophylli* comb. nov.

Jing-Xin Ji[1*A], Zhuang Li[2], Yu Li[1], Makoto Kakishima[1, 3,4*B]

[1] *Engineering Research Center of Chinese Ministry of Education for Edible and Medicinal Fungi, Jilin Agricultural University, Changchun, Jilin 130118, China*

[2] *College of Plant Pathology, Shandong Agricultural University, Tai'an 271000, China*

[3] *College of Forestry, Beijing Forestry University, Beijing 100083, China*

[4] *University of Tsukuba, Tsukuba, Ibaraki 305-8572, Japan*

* Correspondence to: [A]*1096314395@qq.com* [B] *kakishima.makoto.ga@u.tsukuba.ac.jp*

Abstract—Spermogonial and aecial stages of *Aecidium caulophylli* on *Caulophyllum robustum* (*Berberidaceae*) were shown by phylogenetic analyses of ITS and 28S sequence data to be identical to a uredinial and telial rust on *Milium effusum* (*Poaceae*). A new combination, *Puccinia caulophylli* is proposed for this species, and an epitype is designated.

Key words—*Pucciniaceae, Pucciniales,* taxonomy

Introduction

Aecidium caulophylli was described in 1898 based on spermogonial and aecial stages of a specimen on *Caulophyllum robustum* (*Berberidaceae*) collected by V. Komarov in Amur, Siberia, Russian Far East, during June 1895 (Saccardo & Sydow 1902). This rust has been reported from China, Russian Far East, and Japan (Miura 1928, Ito 1950, Tai 1979, Harada 1984, Hiratsuka & al. 1992, Azbukina 2005). However, its uredinial and telial stages have not been clearly demonstrated, although Azbukina (1984, 2005) listed this species as spermogonial and aecial stages of *Puccinia brachypodii* var. *poae-nemoralis* (G.H. Otth) Cummins & H.C. Greene [≡ *P. poae-nemoralis* G.H. Otth], without any evidence.

Table 1. Sequence data analyzed in this study

Species	Host plant	Locality in China	Date	Voucher Specimen	GenBank accession No.	
					ITS	28S
Puccinia caulophylli	*Caulophyllum robustum*	Hongyegu, Jiaohe, Jilin, Jilin	24-Jun-2015	HMJAU8531	MK785259	MK785284
	C. robustum	Lafa Mountain, Jiaohe, Jilin, Jilin	23-Jun-2015	HMJAU8532	MK785260	MK785284
	C. robustum	Bangchuigu, Jiaohe, Jilin, Jilin	1-Jul-2018	HMJAU8624	MK785261	MK785284
	C. robustum	Qingling, Jiaohe, Jilin, Jilin	29-Jun-2017	HMJAU8620	MK785262	MK785284
	C. robustum	Hongyegu, Jiaohe, Jilin, Jilin	24-Jun-2015	HMJAU8534	MK785273	MK785284
	Milium effusum	Fenghuang Mountain, Wuchang, Heilongjiang	5-Jul-2016	HMJAU8619	MK785271	MK785284
	M. effusum	Changbai Mountain, Erdaobaihe, Yanbian, Jilin	28-Jul-2015	HMJAU8618	MK785272	MK785284
	M. effusum	Lushuihe Forest Park, Baishan, Jilin	2-Sep-2018	HMJAU8625	MK785274	MK785284
	M. effusum	Bangchuigu, Jiaohe, Jilin, Jilin	12-Sep-2017	HMJAU8622	MK785275	MK785284
	M. effusum	Erdaobaihe, Yanbian, Jilin	2-Sep-2018	HMJAU8627	MK785276	MK785284
	M. effusum	Lafa Mountain, Jiaohe, Jilin, Jilin	1-Jul-2018	HMJAU8623	MK785277	MK785284
	M. effusum	Lushuihe Forest Park, Baishan, Jilin	3-Sep-2018	HMJAU8626	MK785278	MK785284
	M. effusum	Fenghuang Mountain, Wuchang, Heilongjiang	9-Sep-2017	HMJAU8621	MK785279	MK785284
Puccinia adenocauli	*Carex onoei*	Qingling, Jiaohe, Jilin, Jilin	12-May-2018	HMJAU8630	MK785267	MK785284
	C. onoei	Jilin Agricultural University, Changchun, Jilin	2-Jul-2017	HMJAU8274	MK785268	MK785284
	Adenocaulon himalaicum	Bangchuigu, Jiaohe, Jilin, Jilin	1-Jul-2018	HMJAU8629	MK785269	MK785284
	A. himalaicum	Fenghuang Mountain, Wuchang, Heilongjiang	23-Jun-2017	HMJAU8628	MK785270	MK785284
Puccinia klukistianum	*Ligustrum obtusifolium*	Jilin Agricultural University, Changchun, Jilin	24-Jun-2018	HMJAU8633	MK785263	MK785284
	L. obtusifolium	Jilin Agricultural University, Changchun, Jilin	12-Jun-2015	HMJAU8198	MK785264	MK785284
	L. obtusifolium	Jingyuetan Forest Park, Changchun, Jilin	25-Jun-2017	HMJAU8631	MK785266	MK785284
	Cleistogenes hackelii	Jilin Agricultural University, Changchun, Jilin	28-Aug-2016	HMJAU8282	MK785265	MK785284
	C. hackelii	Jilin Agricultural University, Changchun, Jilin	9-Jul-2016	HMJAU8280	MK785280	MK785284
	C. hackelii	Jingyuetan Forest Park, Changchun, Jilin	16-Sep-2017	HMJAU8632	MK785281	MK785284
Gymnosporangium yamadae	*Malus baccata*	Jilin Agricultural University, Changchun, Jilin	10-Sep-2014	HMJAU8096	MK785282	MK785284
Gymnosporangium asiaticum	*Pyrus* sp.	Wunvfeng Forest Park, Jian, Tonghua, Jilin	8-Jun-2016	HMJAU8324	MK785283	MK785284

During an investigation of rust fungi in Jilin Province, China, during 2015–2018, *A. caulophylli* was observed on *C. robustum*. Near the infected *C. robustum*, uredinial and telial stages of *Puccinia* species were also observed on plants of *Poaceae* and *Cyperaceae*. We suspected that this rust may have an heteromacrocyclic life cycle, producing uredinia and telia on one of these plants. Inoculation of plants with spores is an appropriate method to clarify rust fungus life cycles (Ji & al. 2017a,b), but often plant collection may be restricted in conservation areas. As it may be difficult to supply appropriate growth conditions after transplantation, molecular analyses have been applied to clarify rust life cycles (Liu & Hambleton 2013, Ji & al. 2016, Padamsee & McKenzie 2017, Scholler & al. 2019). We report here the results of phylogenetic and morphological analyses using spermogonial/aecial specimens on *A. caulophylli* and potentially related uredinial/telial specimens on *Poaceae* and *Cyperaceae*.

Materials & methods

Molecular analyses

Spermogonial (0) and aecial (I) stages of *A. caulophylli* on *C. robustum* were collected in Jiaohe, Jilin Province, China, and used for molecular analyses. Rust specimens on *Milium effusum* (*Poaceae*) were collected in several areas in Jilin and Heilongjiang Provinces, China, as preliminary phylogenetic analyses suggested they represented the uredinial (II) and telial (III) stages of *A. caulophylli*. The specimens were collected during surveys of rust fungi in Jilin Province from 2015 to 2018. For comparative analyses, sequences were included from two life cycles that previously clarified by inoculations (Ji & al. 2017a,b): (1) *Puccinia klugkistiana* (Dietel) Jing X. Ji & Kakish. on *Ligustrum obtusifolium* Siebold & Zucc. (0, I) and *Cleistogenes hackelii* (Honda) Honda (II, III), collected in Changchun, Jilin Province; and (2) *P. adenocauli* (Syd. & P. Syd.) Jing X. Ji & Kakish. on *Adenocaulon himalaicum* Edgew. (0, I) and *Carex onoei* Franch. & Sav. (II, III).

Total genomic DNA was directly extracted from about 200 spores obtained from single sori on the leaves of each specimen, using similar methods reported by Ji & al. (2016, 2019). Specimens used in the experiments were deposited in the Herbarium of Mycology, Engineering Research Center of Chinese Ministry of Education for Edible and Medicinal Fungi, Jilin Agricultural University, China (HMJAU) and all data sequenced in this experiment were deposited at GenBank (Table 1).

Sequences from the specimens were aligned following Ji & al. (2019). ITS and 28S sequence data retrieved from GenBank were added to phylogenetic analyses. Accession numbers for these data are shown in the phylogenetic trees (Figs 1, 2). Phylogenetic trees were constructed with the sequences of *Gymnosporangium yamadae* Miyabe ex G. Yamada and *G. asiaticum* Miyabe ex G. Yamada as outgroup,

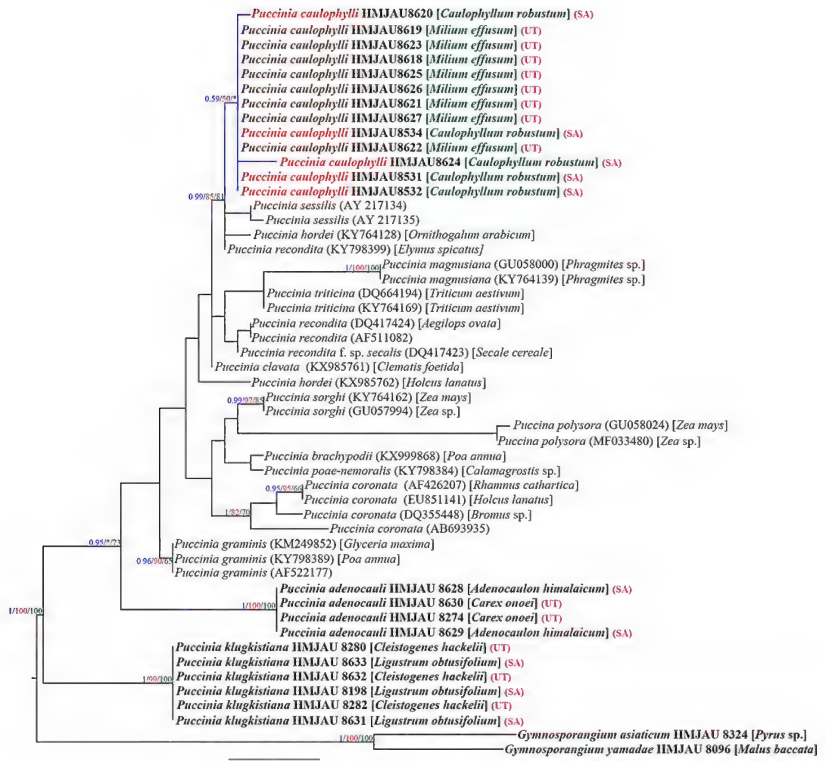
Puccinia caulophylli HMJAU8620 [Caulophyllum robustum] (SA)
Puccinia caulophylli HMJAU8619 [Milium effusum] (UT)
Puccinia caulophylli HMJAU8623 [Milium effusum] (UT)
Puccinia caulophylli HMJAU8618 [Milium effusum] (UT)
Puccinia caulophylli HMJAU8625 [Milium effusum] (UT)
Puccinia caulophylli HMJAU8626 [Milium effusum] (UT)
Puccinia caulophylli HMJAU8621 [Milium effusum] (UT)
Puccinia caulophylli HMJAU8627 [Milium effusum] (UT)
Puccinia caulophylli HMJAU8534 [Caulophyllum robustum] (SA)
Puccinia caulophylli HMJAU8622 [Milium effusum] (UT)
Puccinia caulophylli HMJAU8624 [Caulophyllum robustum] (SA)
Puccinia caulophylli HMJAU8531 [Caulophyllum robustum] (SA)
Puccinia caulophylli HMJAU8532 [Caulophyllum robustum] (SA)
Puccinia sessilis (AY 217134)
Puccinia sessilis (AY 217135)
Puccinia hordei (KY764128) [Ornithogalum arabicum]
Puccinia recondita (KY798399) [Elymus spicatus]
Puccinia magnusiana (GU058000) [Phragmites sp.]
Puccinia magnusiana (KY764139) [Phragmites sp.]
Puccinia triticina (DQ664194) [Triticum aestivum]
Puccinia triticina (KY764169) [Triticum aestivum]
Puccinia recondita (DQ417424) [Aegilops ovata]
Puccinia recondita (AF511082)
Puccinia recondita f. sp. secalis (DQ417423) [Secale cereale]
Puccinia clavata (KX985761) [Clematis foetida]
Puccinia hordei (KX985762) [Holcus lanatus]
Puccinia sorghi (KY764162) [Zea mays]
Puccinia sorghi (GU057994) [Zea sp.]
Puccina polysora (GU058024) [Zea mays]
Puccina polysora (MF033480) [Zea sp.]
Puccinia brachypodii (KX999868) [Poa annua]
Puccinia poae-nemoralis (KY798384) [Calamagrostis sp.]
Puccinia coronata (AF426207) [Rhamnus catharticа]
Puccinia coronata (EU851141) [Holcus lanatus]
Puccinia coronata (DQ355448) [Bromus sp.]
Puccinia coronata (AB693935)
Puccinia graminis (KM249852) [Glyceria maxima]
Puccinia graminis (KY798389) [Poa annua]
Puccinia graminis (AF522177)
Puccinia adenocauli HMJAU 8628 [Adenocaulon himalaicum] (SA)
Puccinia adenocauli HMJAU 8630 [Carex onoei] (UT)
Puccinia adenocauli HMJAU 8274 [Carex onoei] (UT)
Puccinia adenocauli HMJAU 8629 [Adenocaulon himalaicum] (SA)
Puccinia klugkistiana HMJAU 8280 [Cleistogenes hackelii] (UT)
Puccinia klugkistiana HMJAU 8633 [Ligustrum obtusifolium] (SA)
Puccinia klugkistiana HMJAU 8632 [Cleistogenes hackelii] (UT)
Puccinia klugkistiana HMJAU 8198 [Ligustrum obtusifolium] (SA)
Puccinia klugkistiana HMJAU 8282 [Cleistogenes hackelii] (UT)
Puccinia klugkistiana HMJAU 8631 [Ligustrum obtusifolium] (SA)
Gymnosporangium asiaticum HMJAU 8324 [Pyrus sp.]
Gymnosporangium yamadae HMJAU 8096 [Malus baccata]

Fig. 1. Phylogenetic tree constructed by MP method based on sequences of 28S regions of rDNA. Bootstrap values of MP and ML are followed by the Bayesian posterior probabilities (BPP) on the nodes in the topology. Asterisk (*) represents bootstrap values <50% or BPP <0.5 in the topology. Sample data are shown with species name, voucher specimen number or GenBank accession number (in parentheses), and host plant. Sequence data determined in this study are shown in bold face. SA: Spermogonial and aecial stages, UT: Uredinial and telial stages.

according to Ji & al. (2019). The alignment and trees were deposited in TreeBase under http://purl.org/phylo/treebase/phylows/study/TB2:S24307 (Fig. 1) and TB2:S24308 (Fig. 2).

Morphological observations

Light (LM) and scanning electron (SEM) microscopy were used to examine morphological characters of rust specimens including the size and shape of sori and spores following Ji & al. (2019).

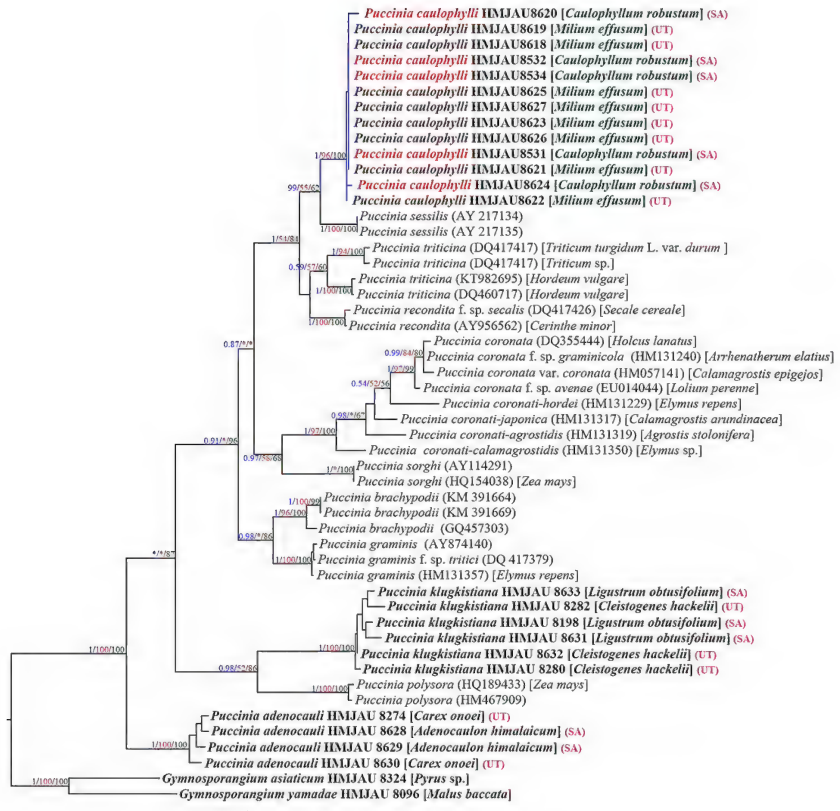
Puccinia caulophylli HMJAU8620 [Caulophyllum robustum] (SA)
Puccinia caulophylli HMJAU8619 [Milium effusum] (UT)
Puccinia caulophylli HMJAU8618 [Milium effusum] (UT)
Puccinia caulophylli HMJAU8532 [Caulophyllum robustum] (SA)
Puccinia caulophylli HMJAU8534 [Caulophyllum robustum] (SA)
Puccinia caulophylli HMJAU8625 [Milium effusum] (UT)
Puccinia caulophylli HMJAU8627 [Milium effusum] (UT)
Puccinia caulophylli HMJAU8623 [Milium effusum] (UT)
Puccinia caulophylli HMJAU8626 [Milium effusum] (UT)
Puccinia caulophylli HMJAU8531 [Caulophyllum robustum] (SA)
Puccinia caulophylli HMJAU8621 [Milium effusum] (UT)
Puccinia caulophylli HMJAU8624 [Caulophyllum robustum] (SA)
Puccinia caulophylli HMJAU8622 [Milium effusum] (UT)
Puccinia sessilis (AY 217134)
Puccinia sessilis (AY 217135)
Puccinia triticina (DQ417417) [Triticum turgidum L. var. durum]
Puccinia triticina (DQ417417) [Triticum sp.]
Puccinia triticina (KT982695) [Hordeum vulgare]
Puccinia triticina (DQ460717) [Hordeum vulgare]
Puccinia recondita f. sp. secalis (DQ417426) [Secale cereale]
Puccinia recondita (AY956562) [Cerinthe minor]
Puccinia coronata (DQ355444) [Holcus lanatus]
Puccinia coronata f. sp. graminicola (HM131240) [Arrhenatherum elatius]
Puccinia coronata var. coronata (HM057141) [Calamagrostis epigejos]
Puccinia coronata f. sp. avenae (EU014044) [Lolium perenne]
Puccinia coronati-hordei (HM131229) [Elymus repens]
Puccinia coronati-japonica (HM131317) [Calamagrostis arundinacea]
Puccinia coronati-agrostidis (HM131319) [Agrostis stolonifera]
Puccinia coronati-calamagrostidis (HM131350) [Elymus sp.]
Puccinia sorghi (AY114291)
Puccinia sorghi (HQ154038) [Zea mays]
Puccinia brachypodii (KM 391664)
Puccinia brachypodii (KM 391669)
Puccinia brachypodii (GQ457303)
Puccinia graminis (AY874140)
Puccinia graminis f. sp. tritici (DQ 417379)
Puccinia graminis (HM131357) [Elymus repens]
Puccinia klugkistiana HMJAU 8633 [Ligustrum obtusifolium] (SA)
Puccinia klugkistiana HMJAU 8282 [Cleistogenes hackelii] (UT)
Puccinia klugkistiana HMJAU 8198 [Ligustrum obtusifolium] (SA)
Puccinia klugkistiana HMJAU 8631 [Ligustrum obtusifolium] (SA)
Puccinia klugkistiana HMJAU 8632 [Cleistogenes hackelii] (UT)
Puccinia klugkistiana HMJAU 8280 [Cleistogenes hackelii] (UT)
Puccinia polysora (HQ189433) [Zea mays]
Puccinia polysora (HM467909)
Puccinia adenocauli HMJAU 8274 [Carex onoei] (UT)
Puccinia adenocauli HMJAU 8628 [Adenocaulon himalaicum] (SA)
Puccinia adenocauli HMJAU 8629 [Adenocaulon himalaicum] (SA)
Puccinia adenocauli HMJAU 8630 [Carex onoei] (UT)
Gymnosporangium asiaticum HMJAU 8324 [Pyrus sp.]
Gymnosporangium yamadae HMJAU 8096 [Malus baccata]

Fig. 2. Phylogenetic tree constructed by MP method based on ITS regions of rDNA. Bootstrap values of MP and ML are followed by the Bayesian posterior probabilities (BPP) on the nodes in the topology. Asterisk (*) represents bootstrap values <50% or BPP <0.5 in the topology. Sample data are shown with species name, voucher specimen number or GenBank accession number (in parentheses), and host plant. Sequence data determined in this study are shown in bold face. SA: Spermogonial and aecial stages, UT: Uredinial and telial stages

Results & discussion

Phylogeny and life cycle

The 28S dataset comprised 51 sequences of 50 taxa with 525 total characters, including 430 constant characters, 25 parsimony-uninformative variable characters, and 70 parsimony-informative characters. Parsimony analysis yielded one parsimonious tree with TL = 159, CI = 0.679, RI = 0.864

and RC = 0.587. Bayesian analysis resulted in average standard deviation of split frequencies of 0.005869. The final ITS dataset comprised 51 sequences of 50 taxa with 820 total characters, of which 336 were parsimony-informative. Parsimony analysis yielded one parsimonious tree with TL = 995, CI = 0.623, RI = 0.840 and RC = 0.523. Bayesian analysis resulted in average standard deviation of split frequencies of 0.004251. Tree topologies formed by MP, ML, and MCMC methods were identical among trees. The phylogenetic trees generated through Bayesian analysis are shown in Fig. 1 (28S) and Fig. 2 (ITS).

Both 28S and ITS phylogenetic trees placed spermogonial and aecial stages on *C. robustum* (HMJAU 8531, 8532, 8534, 8620, 8624) and uredinial and telial stages on *M. effusum* (HMJAU 8618, 8619, 8621, 8622, 8623, 8625, 8626, 8627) within a monophyletic clade (Figs 1, 2). All stages of *P. klugkistiana* and *P. adenocauli* were placed in separate monophyletic clades, confirming that heteroecious life cycles of rust fungi can be revealed by phylogenetic analyses as demonstrated by Liu & Hambleton (2013), Padamsee & McKenzie (2017), and Scholler & al. (2019). The phylogenetic analyses also supported the life cycle connection between the rust on *C. robustum* and the rust on *M. effusum*.

Although the *Caulophyllum/Milium* rust was shown to be phylogenetically close to *P. sessilis* W.G. Schneid. ex J. Schröt., *P. triticina* Erickss., and *P. recondita* Roberge ex Desm., these three rusts inhabit different host plants. This rust is also genetically distant from *P. brachypodii* G.H. Otth and *P. poae-nemoralis,* two other telial rusts reported on *Milium* spp. (Cummins 1971, Zhuang & al. 1998, Azbukina 2005). Therefore, we conclude that this rust is distinct from other species.

Morphology & taxonomy

From the phylogenetic analyses, the spermogonia and aecia on *A. caulophylli* and the uredinia and telia on *M. effusum* are produced by one and the same heteromacrocyclic rust species. LM and SEM observations showed that overall morphology of the rust on *C. robustum* is identical with that of *A. caulophylli* described by Saccardo & Sydow (1902), Ito (1950), Harada (1984), and Hiratsuka & al. (1992) (Figs 3, 5A,B). The morphologies of uredinial and telial specimens on *M. effusum* were similar to each other (Figs 4, 5C–E), and the two-celled teliospores refer the rust to the genus *Puccinia* (Cummins & Hiratsuka 2003).

Specimens on *Milium effusum* are phylogenetically close to *P. sessilis,* but urediniospores on *M. effusum* are bigger than those of *P. sessilis* (20–32

Fig. 3. *Puccinia caulophylli* on *Caulophyllum robustum*: spermogonial and aecial stages. A. Yellow lesions on the leaves producing spermogonia and aecia; B. Aecia produced around spermogonia on lower surface of the plant; C. Catenulate aeciospores surrounded by peridium in a vertical section of an aecium; D. Vertical section of a spermogonium; E. Aeciospores. Scale bars: C, D = 30 μm; E = 15 μm.

× 19–25 μm), and teliospores are smaller than those of *P. sessilis* (32–58 × 13–20 μm). Additionally, the rust on *M. effusum* has uredinial paraphyses that have not been reported in *P. sessilis* (Hiratsuka & al. 1992, Zhuang & al. 1998). *P. brachypodii* var. *poae-nemoralis* occurs on *M. effusum* (Cummins 1971, Zhuang & al. 1998) and its telial structures and teliospores are

morphologically similar to the present rust fungus. However, urediniospores of the current rust are bigger than those of *P. brachypodi*i var. *poae-nemoralis* (18–25 × 15–23 µm). The aecial stage of *P. brachypodi*i var. *poae-nemoralis* occurs on *Berberis* spp. (Cummins 1971).

Aecidium caulophylli is a legitimate name under the International Code of Nomenclature for algae, fungi, and plants (Shenzhen Code, Art. F.8, 2018). However, the application of an asexual name, such as *Aecidium*, to a sexual species can cause confusion (Ono 2016). Therefore, we propose a new combination in *Puccinia* for *A. caulophylli*. The holotype specimen on *C. robustum* has only spermogonial and aecial stages of the rust; because the uredinial and telial stages define the rust genus, we designate an epitype specimen on *M. effusum*.

Puccinia caulophylli (Kom.) Jing X. Ji & Kakish., **comb. nov.** Figs 3–5

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≡ *Aecidium caulophylli* Kom., in Jaczewski & al., Fungi Rossiae Exsicc. 4: no 176, 1898.

Types: Russian Federation, Russian Far East, Siberia, Amur, Mt. Burejenses, stages 0, I on *Caulophyllum robustum* Maxim. [≡ *C. thalictroides* subsp. *robustum* (Maxim.) Kitam.], June 1895, leg. V. Komarov (**holotype**, LE; **isotype**, NY 00610976). China, Jilin Province, Yanbian, *Erdaobaihe*, stages II, III *on Milium effusum* L., 2 September 2018, leg. J.X. Ji & M. Kakishima (**epitype designated here**, HMJAU 8627; MBT 386779).

Spermogonia amphigenous, pale yellow to yellowish brown, subepidermal, type 4 of Cummins & Hiratsuka (2003). Aecia hypophyllous, yellow, subepidermal, erumpent, *Aecidium*-type with firmly connected peridia. Aeciospores catenulate, subglobose, ovate to ellipsoid, 14–24 × 13.5–20 µm (av. 18.5 × 15.5 µm), walls hyaline, 0.5–2 µm thick (av. 1 µm), densely verrucose.

Uredinia mostly hypophyllous, pale yellow to cinnamon-brown, subepidermal, erumpent, with abundant peripheral and intermixed paraphyses. Paraphyses cylindric to capitate, 16.5–41 × 3–9.5 µm (av. 30 × 5 µm), walls hyaline, 0.5–1.5 µm thick (av. 1 µm). Urediniospores pedicellate, globose to subglobose, 22–35 × 21–30.5 µm (av. 30 × 27 µm), walls hyaline or pale yellow, 1–3.5 µm thick (av. 1.5 µm), echinulate, germ pores obscure. Telia mostly hypophyllous, dark brown to black, subepidermal, covered by epidermis, without paraphyses. Teliospores 2-celled by transverse septum, borne singly on pedicels, clavate to oblong, with round to obtuse apex and attenuate towards base, 28.5–40.5 × 9.5–17 µm (av. 35.5 × 13 µm), walls pale brown to dark brown, 0.5–1.5 µm thick at sides (av. 1 µm), 1–5 µm thick at apex (av. 2.5 µm), smooth; pedicels short, hyaline.

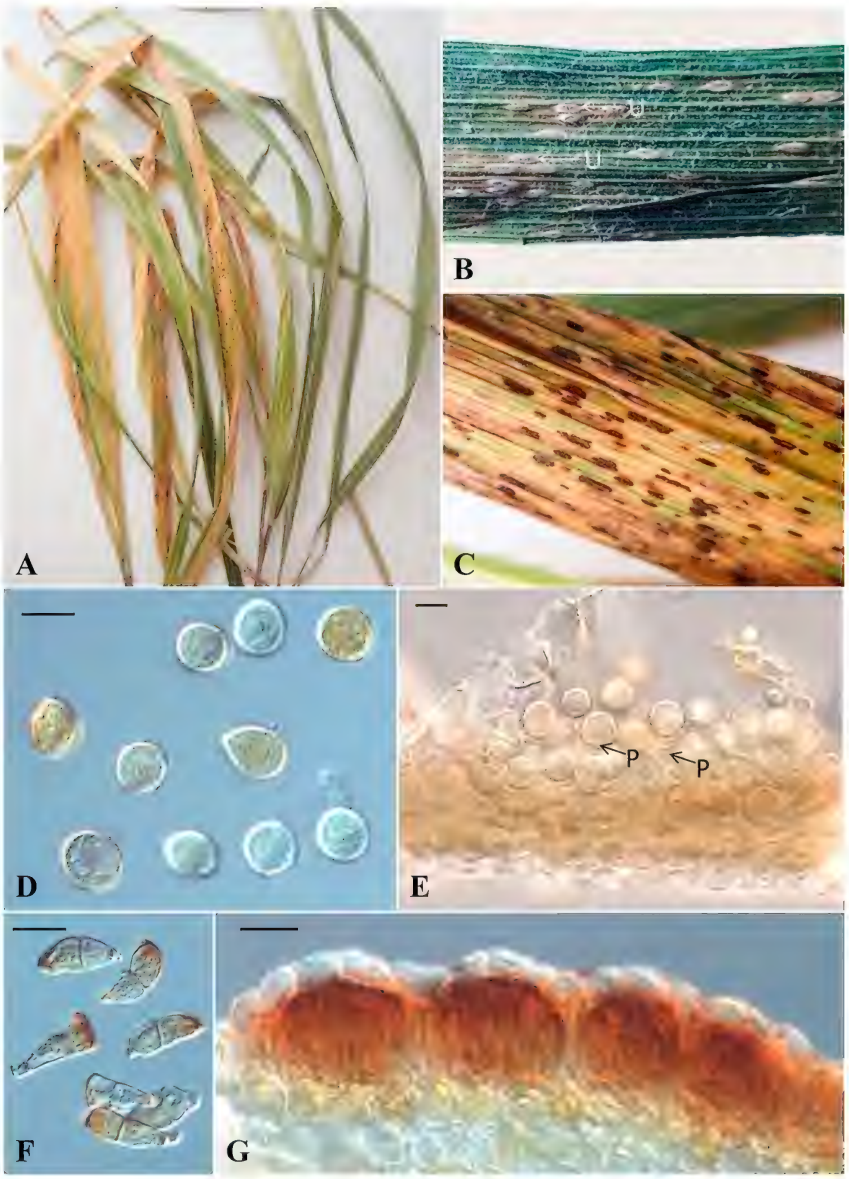

Fig. 4. *Puccinia caulophylli* on *Milium effusum*: uredinial and telial stages. A. Uredinia and telia produced on the leaves; B. Pale yellow uredinia (U) on lower leaf surface; C. Dark brown telia on lower leaf surface; D. Echinulate urediniospores; E. Vertical section of uredinium with urediniospores and paraphyses (P); F. Teliospores; G. Vertical section of telia covered by host epidermis. Scale bars: D, E = 30 µm; F, G = 20 µm.

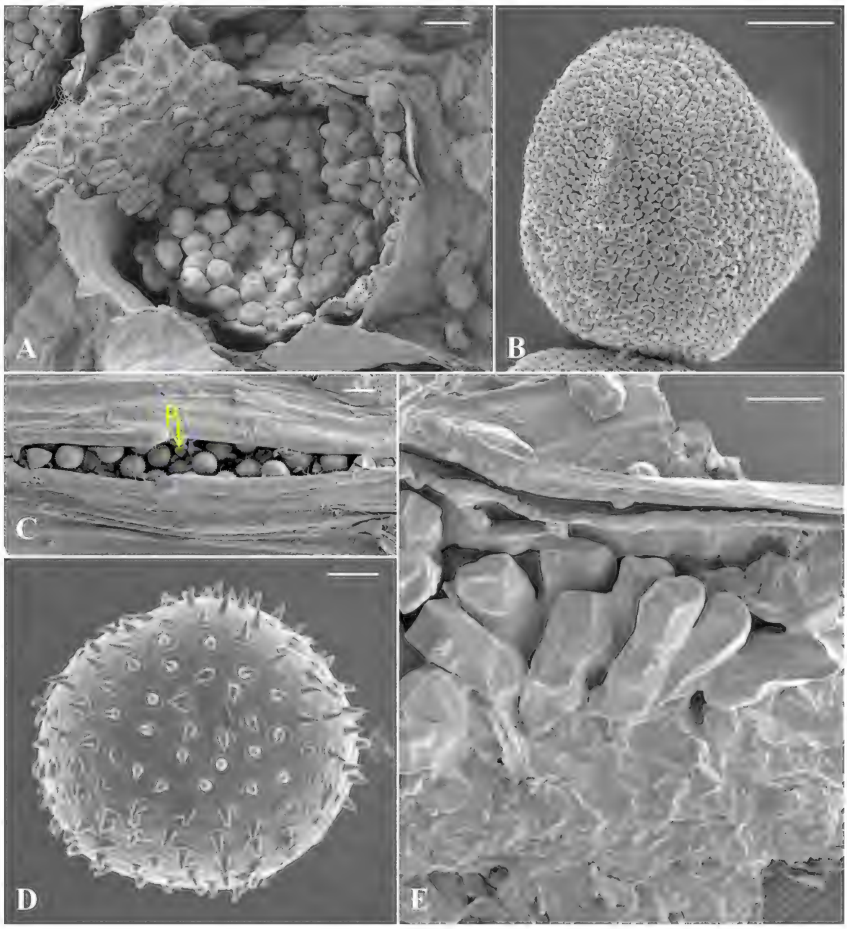

Fig. 5. *Puccinia caulophylli* observed by SEM. A. Aecium with catenulate aeciospores and peridium; B. Aeciospore with densely verrucose surface; C. Uredinium with urediniospores and paraphyses (P); D. Echinulate urediniospore; E. Vertical section of a telium covered by host epidermis. Scale bars: A = 30 μm; B, D = 5 μm; C, E = 20 μm.

Additional specimens examined—**Stages 0, I on *Caulophyllum robustum*: CHINA: Jilin Province, Jilin**, 23 June 2015 (HMJAU 853); 24 June 2015 (HMJAU 8531, HMJAU 8534); 29 June 2017 (HMJAU 8620); 1 July 2018 (HMJAU 8624).

Stages II, III on *Milium effusum*: CHINA: Jilin Province, Jilin, 12 September 2017 (HMJAU 8622); 1 July 2018 (HMJAU 86232). **Yanbian**, 28 July 2015 (HMJAU 8618).; **Baishan**, 2 September 2018 (HMJAU 8625); 3 September 2018 (HMJAU 8626). **Heilongjiang Province: Wuchang**, 5 July 2016 (HMJAU 8619); 9 September 2017 (HMJAU 8621).

HOSTS & DISTRIBUTION—Stages 0, I on *Caulophyllum robustum*: China (Miura 1928, Tai 1979), Japan (Ito 1950, Harada 1984, Hiratsuka & al. 1992). Stages II, III on *Milium effusum*: China.

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Exserticlava aquatica sp. nov., a microfungus from the Brazilian Amazon

Luana Teixeira do Carmo[1], Diogo Careli dos Santos[2], Carolina Ribeiro Silva[2], Sheila Miranda Leão Ferreira[1], Thamara Arão Feletti[1], Luís Fernando Pascholati Gusmão*[1]

[1] *Universidade Estadual de Feira de Santana, Programa de Pós-graduação em Botânica, Av. Transnordestina s/n, Novo Horizonte, 44036-900, Feira de Santana, Brazil*

[2] *Universidade Federal de Pernambuco, Centro de Biociências, Depto de Micología, Av. Prof. Nelson Chaves, s/n, Cidade Universitária, 50670, Recife, Pernambuco, Brazil*

* Correspondence to: *lgusmao@uefs.br*

Abstract—A new species, *Exserticlava aquatica,* collected on submerged decaying twigs in Pará State in the Brazilian Amazon, is described and illustrated. The microfungus is characterized by monoblastic conidiogenesis with repeated percurrent conidiophore extensions and conidiogenous cells with a slightly swollen apex that does not protrude beyond the ruptured outer wall.

Key words—*Ascomycota, Chaetosphaeriaceae,* conidial fungi, freshwater fungi, taxonomy

Introduction

Exserticlava S. Hughes is characterized by distoseptate conidia and a hyaline apical swelling of the conidiogenous cell formed by the inner wall disrupting a pigmented outer wall (Hughes 1978). Tsui & al. (2001) reviewed the morphology of the genus and provided a key to five species; subsequently two more species were described: *E. yunnanensis* and *E. manglietiae* (Cai & Hyde 2007, Ren & al. 2012). *Exserticlava* is associated with the perithecial genus *Chaetosphaeria* Tul. & C. Tul. (Réblová & Seifert 2003, Seifert & al. 2011: 204). During a survey of microfungi associated with twigs in estuary areas, an interesting specimen was collected and is described here as a new *Exserticlava* species.

Material & methods

Samples of submerged decaying twigs were washed in river water to remove sand and placed in plastic bags. In the laboratory, the samples were processed according Castañeda-Ruiz & al. (2016) and regularly examined for 40 days under stereomicroscope for observation of the reproductive structures. Slide mounts were prepared in PVL (polyvinyl alcohol, lactic acid, and phenol) and/or in lactic acid. Microphotographs were obtained using a Olympus BX51 microscope with Nomarski interference optics. The type specimen has been deposited in the Herbarium of Universidade Estadual de Feira de Santana, Brazil (HUEFS).

Taxonomy

Exserticlava aquatica L.T. Carmo, C.R. Silva, Careli, S.M. Leão, Feletti & Gusmão, **sp. nov.** PLATE 1

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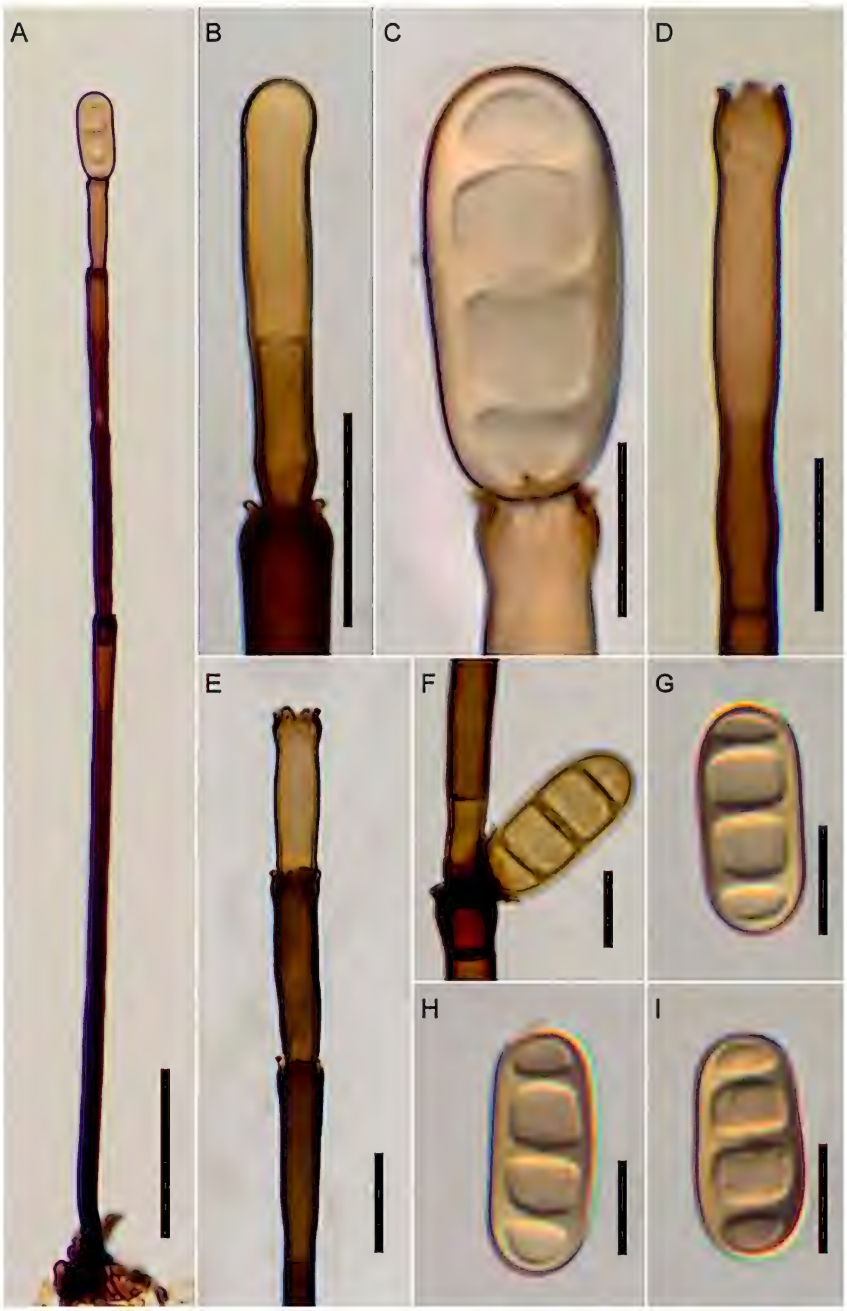
Differs from *Exserticlava triseptata* by its monoblastic conidiogenesis, its conidiogenous cells with a slightly swollen apex that does not protrude beyond the ruptured outer wall, and its smaller oblong-obtuse conidia.

TYPE: Brazil, Pará State: Belém, Mosqueiro island, 1°03′45″S 48°20′14″W, on submerged decaying twigs of unidentified plant, 2.VI.2018, coll. L.T. Carmo (**Holotype,** HUEFS249946).

ETYMOLOGY: the specific epithet refers to the aquatic habitat from which the species was collected.

COLONIES effuse, brown. MYCELIUM superficial and immersed, composed of septate, branched, smooth, pale brown hyphae. CONIDIOPHORES macronematous, mononematous, unbranched, erect, straight or slightly flexuous, smooth, thick-walled, dark brown to paler toward the apex, slightly swollen at the base, surrounded by pseudo-parenchymatous cells forming a brown stroma 22.5–27 µm wide, (6–)8–13–septate, 330–455 × 6.5–7.5 µm. CONIDIOGENOUS CELLS monoblastic, enteroblastic, percurrent and progressive leading to the production of up to 7 conidiogenous cell extensions, integrated, terminal, clavate, slightly swollen at the apex, without conspicuous expansion of the inner wall and not protruding from the fragmented and pigmented outer wall of conidiogenous cells, smooth, pale brown, 18.5–46.5 × 5–7.5 µm. Conidial secession schizolytic. CONIDIA acrogenous, holoblastic, solitary, smooth, oblong-obtuse, thick-walled, 3-distoseptate, sometimes with conspicuous

PLATE 1. *Exserticlava aquatica* (holotype, HUEFS 249946): A. General aspect of conidiophore with attached conidium; B. Conidiogenous cell development; C. Conidium attached to conidiogenous cell; D. Conidiogenous cell; E. Proliferating conidiogenous cells; F. Conidiogenous cell producing a conidium after extension; G–I. Conidia. Scale bars: A = 50 µm; B–I = 10µm.


A
B
C
D
E
F
G
H
I

aperture on distosepta, pale brown, 21–26.5 × 10–11.5 µm; conidia sometimes produced within intercalary old conidiogenous cells. Sexual morph: not observed.

Note: *Exserticlava triseptata*, *E. keniensis*, and *E. vasiformis* most closely resemble *E. aquatica* by producing 3-distoseptate conidia; the four other accepted species are 1-distoseptate (Tsui & al. 2001, Rao & de Hoog 1986). However, *E. triseptata* and *E. keniensis* have brown elliptic-obovoid conidia and the conidiogenous cells extend forming a hyaline swelling that produces conidia; and *E. vasiformis* is distinguished by vigorous inner wall extension of funnel-shaped conidiogenous loci (Hughes 1978, Matsushima 1975, Tsui & al. 2001). *Exserticlava aquatica* is easily separated from the other *Exserticlava* species by its pale brown conidia, its several percurrent conidiogenous cell extensions, and the distinctive crown-like appearance of the outer wall of the conidiogenous cell; the new species is further characterized by monoblastic conidiogenous cells and an absence of conspicuous inner wall expansion to fragment the pigmented outer conidiogenous cell wall.

Exserticlava triseptata and *E. vasiformis* have been widely recorded in Brazil, including in the Amazon region (Cruz & al. 2008).

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Regional annotated mycobiotas new to the Mycotaxon website

Abstract—Mycotaxon is pleased to add to our 'web-list' page the following new annotated species distribution list under South America (Brazil): "*Ascomycota* (lichenized and non-lichenized) on *Syagrus coronata* in the Caatinga biome: new and interesting records for Brazil and South America" by Maiara A.L. dos Santos, Nilo G.S. Fortes, Tássio E.F. Silva, Nadja S. Vitória. This brings to 133 the number of free access Fungae now available on our website: http://www.mycotaxon.com/mycobiota/index.html

SOUTH AMERICA

Brazil

Maiara A.L. dos Santos, Nilo G.S. Fortes, Tássio E.F. Silva, Nadja S. Vitória. *Ascomycota* (lichenized and non-lichenized) on *Syagrus coronata* in the Caatinga biome: new and interesting records for Brazil and South America. 10 p.

Abstract—The Caatinga biome occupies most of the semiarid region of northeastern Brazil, with varied landscapes and notable endemism. Among the plants having significant importance in the Caatinga environment is the palm tree *Syagrus coronata*, which is known as the "life-saving plant" due to its high socio-biological and economic value. To better understand the mycota of the *Arecaceae*, collections were undertaken in the municipalities of Paulo Afonso and Nova Glória within the Raso da Catarina eco-region in the drylands ("sertão") of Bahia State, Brazil. Twenty species of *Ascomycota* were identified during the present work: three are new records for South America (*Diplodia galiicola, Seimatosporium corni*, and *Wojnowiciella viburni*); eleven are new records for Brazil (*Anthostomella caricis*, *Caryospora callicarpa*, *C. putaminum*, *Chaetomium subaffine*, *Diatrype bermudensis*, *Diatrypella persicae*, *Didymosphaeria massarioides*, *Eutypella fraxinicola*, *Munkovalsaria donacina*, *Oedohysterium sinense*, and *Pleospora calvescens*); while six are new records for Bahia State (*Dirinaria confusa*, *Lecanora achroa*, *Phaeosphaeria* sp., *Pleospora herbarum*, *Polymeridium julelloides*, and *Saccardoella macrasca*). *Syagrus coronata* represents a new botanical host for all taxa identified here.

Key words—*Pezizomycotina*, semiarid, taxonomy

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Regional annotated mycobiotas new to the Mycotaxon website

Abstract—Mycotaxon is pleased to add a new annotated species distribution list to our 134 previously posted free access fungae. The 22-page "Checklist of Bolivian *Agaricales*. 1: Species with dark and pink spore prints." by E. Melgarejo-Estrada, M.E. Suárez, D. Rocabado, O. Maillard, and B.E. Lechner may be downloaded from our website via http://www.mycotaxon.com/mycobiota/index.html

South America

Bolivia

E. Melgarejo-Estrada, M.E. Suárez, D. Rocabado, O. Maillard, B.E. Lechner. Checklist of Bolivian *Agaricales*. 1: Species with dark and pink spore prints. 22 p.

Abstract—We provide a literature-based checklist of *Agaricales* reported from Bolivia. In this first contribution, 101 species belonging to 28 genera and 9 families are listed. *Pluteaceae*, *Agaricaceae* and *Hymenogastraceae* are the most species-abundant families.

Key words—*Basidiomycota*, distribution, diversity, *Gasteromycetes*, Neotropics, macromycetes, South America

Exserticlava aquatica sp. nov.

(Carmo & al.— Plate 1, p. 733)